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SEQUENCE LISTING

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 Sauer, Matt
 Klebsattel, Martin
 Flachmann, Ralf

<120> Transgenic expression cassettes for expressing nucleic acids in
 the flower of plants

<130> 13173-00002-US

<150> PCT/EP 03/008394

<151> 2003-07-30

<150> DE 102 38 979.9

<151> 2002-08-20

<150> DE 102 47 599.7

<151> 2002-02-11

<160> 83

<170> PatentIn version 3.3

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<212> DNA

<213> Tagetes erecta

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<221> promoter

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 aattaaaata aagagaagag aaagattaag aggggtgatgg ggatattaaa gacggscaat 180
 atagtgatgc cacgtagaaa aaggtaagtg aaaacatata acgtggcttt aaaagatggc 240
 ttggctgcta atcaactcaa ctcaactcat atcctatcca ttcaaattca attcaattct 300
 attgaatgca aagcaaagca aaggttgttt gttgttggtg ttgagagaca ctccaatcca 360
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 <222> (445)..(537)
 <223> coding for transit peptide of epsilon cyclase

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 atagtgatgc cacgtagaaa aaggtaagtg aaaacatata acgtggcttt aaaagatggc 240
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 aaaaagaatc attactaaca atca atg agt atg aga gct gga cac atg acg 471
 Met Ser Met Arg Ala Gly His Met Thr
 1 5
 gca aca atg gcg gct ttt aca tgc cct agg ttt atg act agc atc aga 519
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 10 15 20 25
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<223> coding for promoter and 5'-UTR region

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gcttggctgc	taatcaactc	aactcaactc	atatactatc	cattcaaatt	caattcaatt	300
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caaacagata	caaggcgtga	ctggatatatt	ctctctcggt	cctaacaaca	gcaacgaaga	420
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<222> (538)..(543)

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<222> (7)..(542)

<223> coding for promoter - 5'-UTR - signal peptide
region

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ttaattaaaa taaagagaag agaaagatta agaggggtgat ggggatatta aagacggsca 180
atatagtgat gccacgtaga aaaaggtaag tgaaaacata caacgtggct ttaaaagatg 240
gcttggctgc taatcaactc aactcaactc atatcctatc cattcaaatt caattcaatt 300
ctattgaatg caaagcaaag caaaggttgt ttgttgttgt tgttgagaga cactccaatc 360
caaacagata caaggcgtga ctggatatct ctctctcggt cctaacaaca gcaacgaaga 420
agaaaaagaa tcattactaa caatcaatga gtatgagagc tggacacatg acggcaacaa 480
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<212> DNA

<213> *Arabidopsis thaliana*

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gctgctgatt cttactacaa tgtggccaca cagacctcgt ttcttcagct gatgaatgat 180
gcgctaattg tctcaaagca aaagggtttc gatgtgttca acgcgttgga tgtgatgcac 240
aatgagagtt tcttgaaaga actgaagttt gggccaggag atggacaact tcattactat 300
ctctacaatt accgtttgaa aagtgccttg aagccagcgg aactcgggct tgttctctta 360
taagctcaac aacttgattt gatggtatca acaaacttga aatttgtctc tctttttttt 420
tcttcagtct gaactacttc tcccatgggt tactgaaact gagtttaatt attttggcaa 480
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<213> *Oryza sativa*

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cctccgttcc accgcgacc cgcgcgcgtc cgttcgcagc gctcgccgt cgccgctccg 480
ctgctgtgca gtcccgccgc cgcgctcgcc ctgactgaag aagaaaagag agaagagaga 540
aaagagaagg gaaggagaag aaaatagaag aaaaaaatat gtgcagctga tgtatgagcc 600
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ccacatactc ttttttaatc ttttttgctg actacgatgc cacgtcagcg aaaccaccta 660
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<222> (141)..(1688)

<223> coding for epsilon-cyclase

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agaatcatta ctaacaatca atg agt atg aga gct gga cac atg acg gca aca 173
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                1         5         10
atg gcg gct ttt aca tgc cct agg ttt atg act agc atc aga tac acg 221
Met Ala Ala Phe Thr Cys Pro Arg Phe Met Thr Ser Ile Arg Tyr Thr
                15         20         25
aag caa att aag tgc aac gct gct aaa agc cag cta gtc gtt aaa caa 269
Lys Gln Ile Lys Cys Asn Ala Ala Lys Ser Gln Leu Val Val Lys Gln
                30         35         40
gag att gag gag gaa gaa gat tat gtg aaa gcc ggt gga tcg gag ctg 317
Glu Ile Glu Glu Glu Glu Asp Tyr Val Lys Ala Gly Gly Ser Glu Leu
                45         50         55
ctt ttt gtt caa atg caa cag aat aag tcc atg gat gca cag tct agc 365
Leu Phe Val Gln Met Gln Gln Asn Lys Ser Met Asp Ala Gln Ser Ser
                60         65         70         75
cta tcc caa aag ctc cca agg gta cca ata gga gga gga gga gac agt 413
Leu Ser Gln Lys Leu Pro Arg Val Pro Ile Gly Gly Gly Gly Asp Ser
                80         85         90
aac tgt ata ctg gat ttg gtt gta att ggt tgt ggt cct gct ggc ctt 461
Asn Cys Ile Leu Asp Leu Val Val Ile Gly Cys Gly Pro Ala Gly Leu
                95         100        105
gct ctt gct gga gaa tca gcc aag cta ggc ttg aat gtc gca ctt atc 509
Ala Leu Ala Gly Glu Ser Ala Lys Leu Gly Leu Asn Val Ala Leu Ile
                110        115        120
ggc cct gat ctt cct ttt aca aat aac tat ggt gtt tgg gag gat gaa 557
Gly Pro Asp Leu Pro Phe Thr Asn Asn Tyr Gly Val Trp Glu Asp Glu
                125        130        135
ttt ata ggt ctt gga ctt gag ggc tgt att gaa cat gtt tgg cga gat 605
Phe Ile Gly Leu Gly Leu Glu Gly Cys Ile Glu His Val Trp Arg Asp
                140        145        150        155
act gta gta tat ctt gat gac aac gat ccc att ctc ata ggt cgt gcc 653
Thr Val Val Tyr Leu Asp Asp Asn Asp Pro Ile Leu Ile Gly Arg Ala
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tat gga cga gtt agt cgt gat tta ctt cac gag gag ttg ttg act agg 701

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Cys	Met	Glu	Ser	Gly	Val	Ser	Tyr	Leu	Ser	Ser	Lys	Val	Glu	Arg	Ile	
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Thr	Glu	Ala	Pro	Asn	Gly	Leu	Ser	Leu	Ile	Glu	Cys	Glu	Gly	Asn	Ile	
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aca	att	cca	tgc	agg	ctt	gct	act	gtc	gct	tct	gga	gca	gct	tct	gga	845
Thr	Ile	Pro	Cys	Arg	Leu	Ala	Thr	Val	Ala	Ser	Gly	Ala	Ala	Ser	Gly	
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aaa	ctt	ttg	cag	tat	gaa	ctt	ggc	ggg	ccc	cgt	gtt	tgc	gtt	caa	aca	893
Lys	Leu	Leu	Gln	Tyr	Glu	Leu	Gly	Gly	Pro	Arg	Val	Cys	Val	Gln	Thr	
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gct	tat	ggg	ata	gag	gtt	gag	gtt	gaa	agc	ata	ccc	tat	gat	cca	agc	941
Ala	Tyr	Gly	Ile	Glu	Val	Glu	Val	Glu	Ser	Ile	Pro	Tyr	Asp	Pro	Ser	
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tca	cta	gaa	gca	caa	tat	cca	aca	ttt	ttg	tat	gtc	atg	cca	atg	tct	1037
Ser	Leu	Glu	Ala	Gln	Tyr	Pro	Thr	Phe	Leu	Tyr	Val	Met	Pro	Met	Ser	
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cca	act	aaa	gta	ttc	ttt	gag	gaa	act	tgt	ttg	gct	tca	aaa	gag	gcc	1085
Pro	Thr	Lys	Val	Phe	Phe	Glu	Glu	Thr	Cys	Leu	Ala	Ser	Lys	Glu	Ala	
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Met	Pro	Phe	Glu	Leu	Leu	Lys	Thr	Lys	Leu	Met	Ser	Arg	Leu	Lys	Thr	
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Met	Gly	Ile	Arg	Ile	Thr	Lys	Thr	Tyr	Glu	Glu	Glu	Trp	Ser	Tyr	Ile	
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cca	gta	ggg	gga	tcc	tta	cca	aat	acc	gag	caa	aag	aac	ctt	gca	ttt	1229
Pro	Val	Gly	Gly	Ser	Leu	Pro	Asn	Thr	Glu	Gln	Lys	Asn	Leu	Ala	Phe	
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Gly	Ala	Ala	Ala	Ser	Met	His	Pro	Ala	Thr	Gly	Tyr	Ser	Val	Val		
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Asp	Leu	Ile	Ile	Phe	Ala	Phe	Tyr	Met	Phe	Ile	Ile	Ala	Pro	His	Ser	
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ctg	aga	atg	ggg	ctg	gtt	aga	cat	ttg	ctt	tct	gac	ccg	aca	gga	gga	1661

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 aca atg tta aaa gcg tat ctc acg ata taaataactc tagtcgcat 1708
 Thr Met Leu Lys Ala Tyr Leu Thr Ile
 510 515
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 <212> PRT
 <213> Tagetes erecta

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 35 40 45
 Glu Asp Tyr Val Lys Ala Gly Gly Ser Glu Leu Leu Phe Val Gln Met
 50 55 60
 Gln Gln Asn Lys Ser Met Asp Ala Gln Ser Ser Leu Ser Gln Lys Leu
 65 70 75 80
 Pro Arg Val Pro Ile Gly Gly Gly Gly Asp Ser Asn Cys Ile Leu Asp
 85 90 95
 Leu Val Val Ile Gly Cys Gly Pro Ala Gly Leu Ala Leu Ala Gly Glu
 100 105 110
 Ser Ala Lys Leu Gly Leu Asn Val Ala Leu Ile Gly Pro Asp Leu Pro
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 Phe Thr Asn Asn Tyr Gly Val Trp Glu Asp Glu Phe Ile Gly Leu Gly
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 Leu Glu Gly Cys Ile Glu His Val Trp Arg Asp Thr Val Val Tyr Leu
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 Asp Asp Asn Asp Pro Ile Leu Ile Gly Arg Ala Tyr Gly Arg Val Ser
 165 170 175
 Arg Asp Leu Leu His Glu Glu Leu Leu Thr Arg Cys Met Glu Ser Gly
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 Val Ser Tyr Leu Ser Ser Lys Val Glu Arg Ile Thr Glu Ala Pro Asn
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 Gly Leu Ser Leu Ile Glu Cys Glu Gly Asn Ile Thr Ile Pro Cys Arg
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 Leu Ala Thr Val Ala Ser Gly Ala Ala Ser Gly Lys Leu Leu Gln Tyr
 225 230 235 240
 Glu Leu Gly Gly Pro Arg Val Cys Val Gln Thr Ala Tyr Gly Ile Glu
 245 250 255
 Val Glu Val Glu Ser Ile Pro Tyr Asp Pro Ser Leu Met Val Phe Met
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 Asp Tyr Arg Asp Tyr Thr Lys His Lys Ser Gln Ser Leu Glu Ala Gln
 275 280 285
 Tyr Pro Thr Phe Leu Tyr Val Met Pro Met Ser Pro Thr Lys Val Phe
 290 295 300
 Phe Glu Glu Thr Cys Leu Ala Ser Lys Glu Ala Met Pro Phe Glu Leu
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<223> coding for epsilon-cyclase
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atg	aga	gct	gga	cac	atg	acg	gca	aca	atg	gcg	gct	ttt	aca	tgc	cct	226		
Met	Arg	Ala	Gly	His	Met	Thr	Ala	Thr	Met	Ala	Ala	Phe	Thr	Cys	Pro			
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agg	ttt	atg	act	agc	atc	aga	tac	acg	aag	caa	att	aag	tgc	aac	gct	274		
Arg	Phe	Met	Thr	Ser	Ile	Arg	Tyr	Thr	Lys	Gln	Ile	Lys	Cys	Asn	Ala			
			20					25				30						
gct	aaa	agc	cag	cta	gtc	ggt	aaa	caa	gag	att	gag	gag	gaa	gaa	gat	322		
Ala	Lys	Ser	Gln	Leu	Val	Val	Lys	Gln	Glu	Ile	Glu	Glu	Glu	Glu	Asp			
			35					40				45				50		
tat	gtg	aaa	gcc	ggt	gga	tcg	gag	ctg	ctt	ttt	ggt	caa	atg	caa	cag	370		
Tyr	Val	Lys	Ala	Gly	Gly	Ser	Glu	Leu	Leu	Phe	Val	Gln	Met	Gln	Gln			
				55						60					65			
aat	aag	tcc	atg	gat	gca	cag	tct	agc	cta	tcc	caa	aag	ctc	cca	agg	418		
Asn	Lys	Ser	Met	Asp	Ala	Gln	Ser	Ser	Leu	Ser	Gln	Lys	Leu	Pro	Arg			
				70					75					80				
gta	cca	ata	gga	gga	gga	gga	gac	agt	aac	tgt	ata	ctg	gat	ttg	gtt	466		
Val	Pro	Ile	Gly	Gly	Gly	Gly	Asp	Ser	Asn	Cys	Ile	Leu	Asp	Leu	Val			
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Val Ile Gly Cys Gly Pro Ala Gly Leu Ala Leu Ala Gly Glu Ser Ala	
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Lys Leu Gly Leu Asn Val Ala Leu Ile Gly Pro Asp Leu Pro Phe Thr	
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Asn Asn Tyr Gly Val Trp Glu Asp Glu Phe Ile Gly Leu Gly Leu Glu	
135 140 145	
ggc tgt att gaa cat gtt tgg cga gat act gta gta tat ctt gat gac	658
Gly Cys Ile Glu His Val Trp Arg Asp Thr Val Val Tyr Leu Asp Asp	
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aac gat ccc att ctc ata ggt cgt gcc tat gga cga gtt agt cgt gat	706
Asn Asp Pro Ile Leu Ile Gly Arg Ala Tyr Gly Arg Val Ser Arg Asp	
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Leu Leu His Glu Glu Leu Leu Thr Arg Cys Met Glu Ser Gly Val Ser	
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Tyr Leu Ser Ser Lys Val Glu Arg Ile Thr Glu Ala Pro Asn Gly Leu	
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agt ctc ata gag tgt gaa ggc aat atc aca att cca tgc agg ctt gct	850
Ser Leu Ile Glu Cys Glu Gly Asn Ile Thr Ile Pro Cys Arg Leu Ala	
215 220 225	
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Thr Val Ala Ser Gly Ala Ala Ser Gly Lys Leu Leu Gln Tyr Glu Leu	
230 235 240	
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Gly Gly Pro Arg Val Cys Val Gln Thr Ala Tyr Gly Tyr Glu Val Glu	
245 250 255	
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Val Glu Ser Ile Pro Tyr Asp Pro Ser Leu Met Val Phe Met Asp Tyr	
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Arg Asp Tyr Thr Lys His Lys Ser Gln Ser Leu Glu Ala Gln Tyr Pro	
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Thr Phe Leu Tyr Val Met Pro Met Ser Pro Thr Lys Val Phe Phe Glu	
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gaa act tgt ttg gct tca aaa gag gcc atg cct ttt gag tta ttg aag	1138
Glu Thr Cys Leu Ala Ser Lys Glu Ala Met Pro Phe Glu Leu Leu Lys	
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Thr Lys Leu Met Ser Arg Leu Lys Thr Met Gly Ile Arg Ile Thr Lys	
325 330 335	
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Thr Tyr Glu Glu Tyr Leu Val Ala Cys Gln Tyr Leu Glu Glu Trp Ser	
340 345 350	
tat att cca gta ggt gga tcc ctt cca aat acc gag caa aag aac ctt	1282
Tyr Ile Pro Val Gly Gly Ser Leu Pro Asn Thr Glu Gln Lys Asn Leu	
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gca ttt ggt gct gct gct agc atg gtg cat cca gcc aca gga tat tcg	1330
Ala Phe Gly Ala Ala Ser Met Val His Pro Ala Thr Gly Tyr Ser	
375 380 385	
ggt gta aga tca ctg tca gaa gct cct aat tat gca gca gta att gca	1378
Val Val Arg Ser Leu Ser Glu Ala Pro Asn Tyr Ala Ala Val Ile Ala	
390 395 400	
aag att tta ggg aaa gga aat tca aaa cag atg ctt gat ctt gga aga	1426
Lys Ile Leu Gly Lys Gly Asn Ser Lys Gln Met Leu Asp Leu Gly Arg	
405 410 415	

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Tyr Thr Thr Asn Ile Ser Lys Gln Ala Trp Glu Thr Leu Trp Pro Leu
420 425 430
gaa agg aaa aga cag aga gca ttc ttt ctc ttt gga tta gca ctg att 1522
Glu Arg Lys Arg Gln Arg Ala Phe Phe Leu Phe Gly Leu Ala Leu Ile
435 440 445 450
gtc cag atg gat att gag ggg acc cgc aca ttc ttc cgg act ttc ttc 1570
Val Gln Met Asp Ile Glu Gly Thr Arg Thr Phe Phe Arg Thr Phe Phe
455 460 465
cgc ttg ccc aca tgg atg tgg tgg ggg ttt ctt gga tct tcg tta tca 1618
Arg Leu Pro Thr Trp Met Trp Trp Gly Phe Leu Gly Ser Ser Leu Ser
470 475 480
tca act gac ttg ata ata ttt gcg ttt tac atg ttt atc ata gca ccg 1666
Ser Thr Asp Leu Ile Ile Phe Ala Phe Tyr Met Phe Ile Ile Ala Pro
485 490 495
cat agc ctg aga atg ggt ctg gtt aga cat ttg ctt tct gac ccg aca 1714
His Ser Leu Arg Met Gly Leu Val Arg His Leu Leu Ser Asp Pro Thr
500 505 510
gga gga aca atg tta aaa gcg tat ctc acg ata taaataactc tagtcgcgat 1767
Gly Gly Thr Met Leu Lys Ala Tyr Leu Thr Ile
515 520 525
cagtttagat tataggcaca tcttgcatat atatatgtat aaaccttatg tgtgctgtat 1827
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<210> 12
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 <212> PRT
 <213> *Tagetes erecta*

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35 40 45
Glu Asp Tyr Val Lys Ala Gly Gly Ser Glu Leu Leu Phe Val Gln Met
50 55 60
Gln Gln Asn Lys Ser Met Asp Ala Gln Ser Ser Leu Ser Gln Lys Leu
65 70 75 80
Pro Arg Val Pro Ile Gly Gly Gly Gly Asp Ser Asn Cys Ile Leu Asp
85 90 95
Leu Val Val Ile Gly Cys Gly Pro Ala Gly Leu Ala Leu Ala Gly Glu
100 105 110
Ser Ala Lys Leu Gly Leu Asn Val Ala Leu Ile Gly Pro Asp Leu Pro
115 120 125
Phe Thr Asn Asn Tyr Gly Val Trp Glu Asp Glu Phe Ile Gly Leu Gly
130 135 140
Leu Glu Gly Cys Ile Glu His Val Trp Arg Asp Thr Val Val Tyr Leu
145 150 155 160
Asp Asp Asn Asp Pro Ile Leu Ile Gly Arg Ala Tyr Gly Arg Val Ser
165 170 175
Arg Asp Leu Leu His Glu Glu Leu Leu Thr Arg Cys Met Glu Ser Gly
180 185 190
Val Ser Tyr Leu Ser Ser Lys Val Glu Arg Ile Thr Glu Ala Pro Asn
195 200 205
Gly Leu Ser Leu Ile Glu Cys Glu Gly Asn Ile Thr Ile Pro Cys Arg

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Glu Leu Gly Gly Pro Arg Val Cys Val Gln Thr Ala Tyr Gly Tyr Glu		240
	245	250
Val Glu Val Glu Ser Ile Pro Tyr Asp Pro Ser Leu Met Val Phe Met		255
	260	265
Asp Tyr Arg Asp Tyr Thr Lys His Lys Ser Gln Ser Leu Glu Ala Gln		270
	275	280
Tyr Pro Thr Phe Leu Tyr Val Met Pro Met Ser Pro Thr Lys Val Phe		285
	290	295
Phe Glu Glu Thr Cys Leu Ala Ser Lys Glu Ala Met Pro Phe Glu Leu		300
305	310	315
Leu Lys Thr Lys Leu Met Ser Arg Leu Lys Thr Met Gly Ile Arg Ile		320
	325	330
Thr Lys Thr Tyr Glu Glu Tyr Leu Val Ala Cys Gln Tyr Leu Glu Glu		335
	340	345
Trp Ser Tyr Ile Pro Val Gly Gly Ser Leu Pro Asn Thr Glu Gln Lys		350
	355	360
Asn Leu Ala Phe Gly Ala Ala Ala Ser Met Val His Pro Ala Thr Gly		365
	370	375
Tyr Ser Val Val Arg Ser Leu Ser Glu Ala Pro Asn Tyr Ala Ala Val		380
385	390	395
Ile Ala Lys Ile Leu Gly Lys Gly Asn Ser Lys Gln Met Leu Asp Leu		400
	405	410
Gly Arg Tyr Thr Thr Asn Ile Ser Lys Gln Ala Trp Glu Thr Leu Trp		415
	420	425
Pro Leu Glu Arg Lys Arg Gln Arg Ala Phe Phe Leu Phe Gly Leu Ala		430
	435	440
Leu Ile Val Gln Met Asp Ile Glu Gly Thr Arg Thr Phe Phe Arg Thr		445
	450	455
Phe Phe Arg Leu Pro Thr Trp Met Trp Trp Gly Phe Leu Gly Ser Ser		460
465	470	475
Leu Ser Ser Thr Asp Leu Ile Ile Phe Ala Phe Tyr Met Phe Ile Ile		480
	485	490
Ala Pro His Ser Leu Arg Met Gly Leu Val Arg His Leu Leu Ser Asp		495
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<220>

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<222> (104)..(1675)

<223> coding for epsilon-cyclase

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 Met Glu Cys Val

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ggg gct agg aat ttc gca gca atg gcg gtt tca aca ttt ccg tca tgg 163
 Gly Ala Arg Asn Phe Ala Ala Met Ala Val Ser Thr Phe Pro Ser Trp
 5 10 15 20

agt	tgt	cga	agg	aaa	ttt	cca	gtg	gtt	aag	aga	tac	agc	tat	agg	aat	211
Ser	Cys	Arg	Arg	Lys	Phe	Pro	Val	Val	Lys	Arg	Tyr	Ser	Tyr	Arg	Asn	
				25					30					35		
att	cgt	ttc	ggg	ttg	tgt	agt	gtc	aga	gct	agc	ggc	ggc	gga	agt	tcc	259
Ile	Arg	Phe	Gly	Leu	Cys	Ser	Val	Arg	Ala	Ser	Gly	Gly	Gly	Ser	Ser	
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ggg	agt	gag	agt	tgt	gta	gcg	gtg	aga	gaa	gat	ttc	gct	gac	gaa	gaa	307
Gly	Ser	Glu	Ser	Cys	Val	Ala	Val	Arg	Glu	Asp	Phe	Ala	Asp	Glu	Glu	
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gat	ttt	gtg	aaa	gct	ggg	ggg	tct	gag	att	cta	ttt	gtt	caa	atg	cag	355
Asp	Phe	Val	Lys	Ala	Gly	Gly	Ser	Glu	Ile	Leu	Phe	Val	Gln	Met	Gln	
	70					75					80					
cag	aac	aaa	gat	atg	gat	gaa	cag	tct	aag	ctt	gtt	gat	aag	ttg	cct	403
Gln	Asn	Lys	Asp	Met	Asp	Glu	Gln	Ser	Lys	Leu	Val	Asp	Lys	Leu	Pro	
	85				90				95						100	
cct	ata	tca	att	ggg	gat	ggg	gct	ttg	gat	cta	gtg	gtt	att	ggg	tgt	451
Pro	Ile	Ser	Ile	Gly	Asp	Gly	Ala	Leu	Asp	Leu	Val	Val	Ile	Gly	Cys	
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Gly	Pro	Ala	Gly	Leu	Ala	Leu	Ala	Ala	Glu	Ser	Ala	Lys	Leu	Gly	Leu	
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Lys	Val	Gly	Leu	Ile	Gly	Pro	Asp	Leu	Pro	Phe	Thr	Asn	Asn	Tyr	Gly	
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His	Val	Trp	Arg	Glu	Thr	Ile	Val	Tyr	Leu	Asp	Asp	Asp	Lys	Pro	Ile	
	165				170				175						180	
acc	att	ggc	cgt	gct	tat	gga	aga	gtt	agt	cga	cgt	ttg	ctc	cat	gag	691
Thr	Ile	Gly	Arg	Ala	Tyr	Gly	Arg	Val	Ser	Arg	Arg	Leu	Leu	His	Glu	
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gag	ctt	ttg	agg	agg	tgt	gtc	gag	tca	ggg	gtc	tcg	tac	ctt	agc	tcg	739
Glu	Leu	Leu	Arg	Arg	Cys	Val	Glu	Ser	Gly	Val	Ser	Tyr	Leu	Ser	Ser	
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Lys	Val	Asp	Ser	Ile	Thr	Glu	Ala	Ser	Asp	Gly	Leu	Arg	Leu	Val	Ala	
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tgt	gac	gac	aat	aac	gtc	att	ccc	tgc	agg	ctt	gcc	act	gtt	gct	tct	835
Cys	Asp	Asp	Asn	Asn	Val	Ile	Pro	Cys	Arg	Leu	Ala	Thr	Val	Ala	Ser	
	230					235					240					
gga	gca	gct	tcg	gga	aag	ctc	ttg	caa	tac	gaa	gtt	ggg	gga	cct	aga	883
Gly	Ala	Ala	Ser	Gly	Lys	Leu	Leu	Gln	Tyr	Glu	Val	Gly	Gly	Pro	Arg	
	245				250					255					260	
gtc	tgt	gtg	caa	act	gca	tac	ggc	gtg	gag	gtt	gag	gtg	gaa	aat	agt	931
Val	Cys	Val	Gln	Thr	Ala	Tyr	Gly	Val	Glu	Val	Glu	Val	Glu	Asn	Ser	
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cca	tat	gat	cca	gat	caa	atg	gtt	ttc	atg	gat	tac	aga	gat	tat	act	979
Pro	Tyr	Asp	Pro	Asp	Gln	Met	Val	Phe	Met	Asp	Tyr	Arg	Asp	Tyr	Thr	
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aac	gag	aaa	gtt	cgg	agc	tta	gaa	gct	gag	tat	cca	acg	ttt	ctg	tac	1027
Asn	Glu	Lys	Val	Arg	Ser	Leu	Glu	Ala	Glu	Tyr	Pro	Thr	Phe	Leu	Tyr	
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gcc	atg	cct	atg	aca	aag	tca	aga	ctc	ttc	ttc	gag	gag	aca	tgt	ttg	1075
Ala	Met	Pro	Met	Thr	Lys	Ser	Arg	Leu	Phe	Phe	Glu	Glu	Thr	Cys	Leu	
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gcc	tca	aaa	gat	gtc	atg	ccc	ttt	gat	ttg	cta	aaa	acg	aag	ctc	atg	1123
Ala	Ser	Lys	Asp	Val	Met	Pro	Phe	Asp	Leu	Leu	Lys	Thr	Lys	Leu	Met	
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Leu Arg Leu Asp Thr Leu Gly Ile Arg Ile Leu Lys Thr Tyr Glu Glu
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Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser Leu Pro Asn Thr Glu Gln
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aag aat ctc gcc ttt ggt gct gcc gct agc atg gta cat ccc gca aca 1267
Lys Asn Leu Ala Phe Gly Ala Ala Ala Ser Met Val His Pro Ala Thr
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ggc tat tca gtt gtg aga tct ttg tct gaa gct cca aaa tat gca tca 1315
Gly Tyr Ser Val Val Arg Ser Leu Ser Glu Ala Pro Lys Tyr Ala Ser
      390                      395                      400
gtc atc gca gag ata cta aga gaa gag act acc aaa cag atc aac agt 1363
Val Ile Ala Glu Ile Leu Arg Glu Glu Thr Thr Lys Gln Ile Asn Ser
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aat att tca aga caa gct tgg gat act tta tgg cca cca gaa agg aaa 1411
Asn Ile Ser Arg Gln Ala Trp Asp Thr Leu Trp Pro Pro Glu Arg Lys
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aga cag aga gca ttc ttt ctc ttt ggt ctt gca ctc ata gtt caa ttc 1459
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gat acc gaa ggc att aga agc ttc ttc cgt act ttc ttc cgc ctt cca 1507
Asp Thr Glu Gly Ile Arg Ser Phe Phe Arg Thr Phe Phe Arg Leu Pro
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aaa tgg atg tgg caa ggg ttt cta gga tca aca tta aca tca gga gat 1555
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Arg Lys Gly Leu Ile Asn His Leu Ile Ser Asp Pro Thr Gly Ala Thr
      505                      510                      515
atg ata aaa acc tat ctc aaa gta tgatttactt atcaactctt aggtttgtgt 1705
Met Ile Lys Thr Tyr Leu Lys Val
      520
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<211> 524

<212> PRT

<213> Arabidopsis thaliana

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Ser Tyr Arg Asn Ile Arg Phe Gly Leu Cys Ser Val Arg Ala Ser Gly
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Gly Gly Ser Ser Gly Ser Glu Ser Cys Val Ala Val Arg Glu Asp Phe
      50          55          60
Ala Asp Glu Glu Asp Phe Val Lys Ala Gly Gly Ser Glu Ile Leu Phe
      65          70          75          80
Val Gln Met Gln Gln Asn Lys Asp Met Asp Glu Gln Ser Lys Leu Val
      85          90          95
Asp Lys Leu Pro Pro Ile Ser Ile Gly Asp Gly Ala Leu Asp Leu Val

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Glu	Thr	Cys	Leu	Ala	Ser	Lys	Asp	Val	Met	Pro	Phe	Asp	Leu	Leu	Lys	
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Thr	Lys	Leu	Met	Leu	Arg	Leu	Asp	Thr	Leu	Gly	Ile	Arg	Ile	Leu	Lys	
			340					345					350			
Thr	Tyr	Glu	Glu	Glu	Trp	Ser	Tyr	Ile	Pro	Val	Gly	Gly	Ser	Leu	Pro	
		355					360					365				
Asn	Thr	Glu	Gln	Lys	Asn	Leu	Ala	Phe	Gly	Ala	Ala	Ala	Ser	Met	Val	
	370					375					380					
His	Pro	Ala	Thr	Gly	Tyr	Ser	Val	Val	Arg	Ser	Leu	Ser	Glu	Ala	Pro	
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Lys	Tyr	Ala	Ser	Val	Ile	Ala	Glu	Ile	Leu	Arg	Glu	Glu	Thr	Thr	Lys	
				405					410					415		
Gln	Ile	Asn	Ser	Asn	Ile	Ser	Arg	Gln	Ala	Trp	Asp	Thr	Leu	Trp	Pro	
			420					425					430			
Pro	Glu	Arg	Lys	Arg	Gln	Arg	Ala	Phe	Phe	Leu	Phe	Gly	Leu	Ala	Leu	
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<211> 1623

<212> DNA

<213> Oryza sativa

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 <222> (1)..(1620)
 <223> coding for epsilon-cyclase

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Arg Ala Ala Trp Gly Ala Ala Ala Ala Gly Ala Gly Ala Glu Gly Arg	
20 25 30	
agc agg agg gtt gtg ccg cgc gcg gtg gag ccg cgg cgg cgc ggg cgg	144
Ser Arg Arg Val Val Pro Arg Ala Val Glu Pro Arg Arg Arg Gly Arg	
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Trp Met Val Arg Cys Val Ala Thr Glu Lys His Lys Asp Ala Ala Ala	
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Lys Gly Gly Gly Gly Glu Leu Leu Tyr Val Gln Met Gln Ala Ser Lys	
85 90 95	
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Ser Met Asp Ser Gln Ser Lys Ile Ser Ser Lys Leu Leu Pro Ile Pro	
100 105 110	
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Asp Glu Asn Ser Val Leu Asp Leu Val Ile Ile Gly Cys Gly Pro Ala	
115 120 125	
ggc tta tcc cta gca gca gag tca gct aag aaa ggg ctc aat gtt ggt	432
Gly Leu Ser Leu Ala Ala Glu Ser Ala Lys Lys Gly Leu Asn Val Gly	
130 135 140	
ctc att ggc cct gat ctt cca ttc acg aac aac tac ggt gtg tgg gag	480
Leu Ile Gly Pro Asp Leu Pro Phe Thr Asn Asn Tyr Gly Val Trp Glu	
145 150 155 160	
gat gaa ttc aaa gac ctg ggc ctg gag agc tgc att gaa cat gtc tgg	528
Asp Glu Phe Lys Asp Leu Gly Leu Glu Ser Cys Ile Glu His Val Trp	
165 170 175	
aag gat act atc gtg tac cta gac ggt aac aag cca ata atg att ggc	576
Lys Asp Thr Ile Val Tyr Leu Asp Gly Asn Lys Pro Ile Met Ile Gly	
180 185 190	
cgt gcg tat ggc agg gtt cac agg gac ttg ctg cac gag gag ttg ctg	624
Arg Ala Tyr Gly Arg Val His Arg Asp Leu Leu His Glu Glu Leu Leu	
195 200 205	
aga cga tgc tat gac gct ggc gtc aca tac ctc agc tcg aag gtg gac	672
Arg Arg Cys Tyr Asp Ala Gly Val Thr Tyr Leu Ser Ser Lys Val Asp	
210 215 220	
aag atc atg gaa tct cct gat gga cat cgg gta gtc tgt tgt gaa ggg	720
Lys Ile Met Glu Ser Pro Asp Gly His Arg Val Val Cys Cys Glu Gly	
225 230 235 240	
gat cgt gag gta ctt tgc agg ctt gcc att gtt gca tct ggg gca gca	768
Asp Arg Glu Val Leu Cys Arg Leu Ala Ile Val Ala Ser Gly Ala Ala	
245 250 255	
tct ggt agg ctt cta gag tac gag gtt ggt ggt ccg cgt gtt tgt gtg	816
Ser Gly Arg Leu Leu Glu Tyr Glu Val Gly Gly Pro Arg Val Cys Val	
260 265 270	
cag act gca tat ggt gtc gaa gtc gag gtg gaa aac aat cca tat gat	864
Gln Thr Ala Tyr Gly Val Glu Val Glu Val Glu Asn Asn Pro Tyr Asp	

	275		280		285	
ccc agc tta atg gtt ttc atg gac tac aga gat tgc ttc aaa gac aaa						912
Pro Ser Leu Met Val Phe Met Asp Tyr Arg Asp Cys Phe Lys Asp Lys						
290		295		300		
ttc tca cat cct gag caa gga aat cca acg ttc ctc tat gcc atg ccc						960
Phe Ser His Pro Glu Gln Gly Asn Pro Thr Phe Leu Tyr Ala Met Pro						
305		310		315		320
atg tca tcc aca cga att ttc ttt gag gaa aca tgc cta gct tct aaa						1008
Met Ser Ser Thr Arg Ile Phe Phe Glu Glu Thr Cys Leu Ala Ser Lys						
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gaa gca atg ccc ttt gac ctc ctt aaa aag cgg ttg atg tct cgg ttg						1056
Glu Ala Met Pro Phe Asp Leu Leu Lys Lys Arg Leu Met Ser Arg Leu						
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gat gca atg gga gtt cat att cga aaa gta tac gag gag gaa tgg tcc						1104
Asp Ala Met Gly Val His Ile Arg Lys Val Tyr Glu Glu Glu Trp Ser						
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tac att cct gtt gga ggg tcc tta cca aat aca gac cag aaa aat ctc						1152
Tyr Ile Pro Val Gly Gly Ser Leu Pro Asn Thr Asp Gln Lys Asn Leu						
	370		375		380	
gca ttt ggt gcg gca gca agt atg gtg cat cct gca acc gga tac tcg						1200
Ala Phe Gly Ala Ala Ala Ser Met Val His Pro Ala Thr Gly Tyr Ser						
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gtg gtt aga tca ttg tct gaa gct cca aga tat gca tct gtg ata tct						1248
Val Val Arg Ser Leu Ser Glu Ala Pro Arg Tyr Ala Ser Val Ile Ser						
	405		410		415	
gat atc ttg aga aac cgt gtc tac cct gga gaa tat ttg cct gga acc						1296
Asp Ile Leu Arg Asn Arg Val Tyr Pro Gly Glu Tyr Leu Pro Gly Thr						
	420		425		430	
tct caa agt tcc agt cca tca atg ctt gca tgg aga aca tta tgg ccc						1344
Ser Gln Ser Ser Ser Pro Ser Met Leu Ala Trp Arg Thr Leu Trp Pro						
	435		440		445	
caa gaa cgg aaa cgt caa cga tca ttc ttc ctt ttt ggg ctg gct ttg						1392
Gln Glu Arg Lys Arg Gln Arg Ser Phe Phe Leu Phe Gly Leu Ala Leu						
	450		455		460	
ata atc caa ctg aat aac gaa ggc att cag aca ttc ttt gaa acc ttt						1440
Ile Ile Gln Leu Asn Asn Glu Gly Ile Gln Thr Phe Phe Glu Thr Phe						
	465		470		475	480
ttc cgg ttg ccc aaa tgg atg tgg cga gga ttc ctt ggt tcg acg ctt						1488
Phe Arg Leu Pro Lys Trp Met Trp Arg Gly Phe Leu Gly Ser Thr Leu						
	485		490		495	
tct tca gtg gat ctc ata ctc ttt gca ttc tac atg ttc aca att gcg						1536
Ser Ser Val Asp Leu Ile Leu Phe Ala Phe Tyr Met Phe Thr Ile Ala						
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ccg aac caa atg cga atg aac ctt gtc aga cat ctc ctc tct gat ccg						1584
Pro Asn Gln Met Arg Met Asn Leu Val Arg His Leu Leu Ser Asp Pro						
	515		520		525	
acc ggc tca acg atg atc aag acc tac ctg acc ttg taa						1623
Thr Gly Ser Thr Met Ile Lys Thr Tyr Leu Thr Leu						
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<211> 540

<212> PRT

<213> Oryza sativa

<400> 16

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Arg	Ala	Ala	Trp	Gly	Ala	Ala	Ala	Ala	Gly	Ala	Gly	Ala	Glu	Gly	Arg	20	25	30
Ser	Arg	Arg	Val	Val	Pro	Arg	Ala	Val	Glu	Pro	Arg	Arg	Arg	Gly	Arg	35	40	45
Trp	Met	Val	Arg	Cys	Val	Ala	Thr	Glu	Lys	His	Lys	Asp	Ala	Ala	Ala	50	55	60
Arg	Arg	Gly	Gly	Val	Glu	Val	Glu	Phe	Ala	Asp	Glu	Glu	Asp	Tyr	Val	65	70	75
Lys	Gly	Gly	Gly	Gly	Glu	Leu	Leu	Tyr	Val	Gln	Met	Gln	Ala	Ser	Lys	85	90	95
Ser	Met	Asp	Ser	Gln	Ser	Lys	Ile	Ser	Ser	Lys	Leu	Leu	Pro	Ile	Pro	100	105	110
Asp	Glu	Asn	Ser	Val	Leu	Asp	Leu	Val	Ile	Ile	Gly	Cys	Gly	Pro	Ala	115	120	125
Gly	Leu	Ser	Leu	Ala	Ala	Glu	Ser	Ala	Lys	Lys	Gly	Leu	Asn	Val	Gly	130	135	140
Leu	Ile	Gly	Pro	Asp	Leu	Pro	Phe	Thr	Asn	Asn	Tyr	Gly	Val	Trp	Glu	145	150	155
Asp	Glu	Phe	Lys	Asp	Leu	Gly	Leu	Glu	Ser	Cys	Ile	Glu	His	Val	Trp	165	170	175
Lys	Asp	Thr	Ile	Val	Tyr	Leu	Asp	Gly	Asn	Lys	Pro	Ile	Met	Ile	Gly	180	185	190
Arg	Ala	Tyr	Gly	Arg	Val	His	Arg	Asp	Leu	Leu	His	Glu	Glu	Leu	Leu	195	200	205
Arg	Arg	Cys	Tyr	Asp	Ala	Gly	Val	Thr	Tyr	Leu	Ser	Ser	Lys	Val	Asp	210	215	220
Lys	Ile	Met	Glu	Ser	Pro	Asp	Gly	His	Arg	Val	Val	Cys	Cys	Glu	Gly	225	230	235
Asp	Arg	Glu	Val	Leu	Cys	Arg	Leu	Ala	Ile	Val	Ala	Ser	Gly	Ala	Ala	245	250	255
Ser	Gly	Arg	Leu	Leu	Glu	Tyr	Glu	Val	Gly	Gly	Pro	Arg	Val	Cys	Val	260	265	270
Gln	Thr	Ala	Tyr	Gly	Val	Glu	Val	Glu	Val	Glu	Asn	Asn	Pro	Tyr	Asp	275	280	285
Pro	Ser	Leu	Met	Val	Phe	Met	Asp	Tyr	Arg	Asp	Cys	Phe	Lys	Asp	Lys	290	295	300
Phe	Ser	His	Pro	Glu	Gln	Gly	Asn	Pro	Thr	Phe	Leu	Tyr	Ala	Met	Pro	305	310	315
Met	Ser	Ser	Thr	Arg	Ile	Phe	Phe	Glu	Glu	Thr	Cys	Leu	Ala	Ser	Lys	325	330	335
Glu	Ala	Met	Pro	Phe	Asp	Leu	Leu	Lys	Lys	Arg	Leu	Met	Ser	Arg	Leu	340	345	350
Asp	Ala	Met	Gly	Val	His	Ile	Arg	Lys	Val	Tyr	Glu	Glu	Glu	Trp	Ser	355	360	365
Tyr	Ile	Pro	Val	Gly	Gly	Ser	Leu	Pro	Asn	Thr	Asp	Gln	Lys	Asn	Leu	370	375	380
Ala	Phe	Gly	Ala	Ala	Ala	Ser	Met	Val	His	Pro	Ala	Thr	Gly	Tyr	Ser	385	390	395
Val	Val	Arg	Ser	Leu	Ser	Glu	Ala	Pro	Arg	Tyr	Ala	Ser	Val	Ile	Ser	405	410	415
Asp	Ile	Leu	Arg	Asn	Arg	Val	Tyr	Pro	Gly	Glu	Tyr	Leu	Pro	Gly	Thr	420	425	430
Ser	Gln	Ser	Ser	Ser	Pro	Ser	Met	Leu	Ala	Trp	Arg	Thr	Leu	Trp	Pro	435	440	445
Gln	Glu	Arg	Lys	Arg	Gln	Arg	Ser	Phe	Phe	Leu	Phe	Gly	Leu	Ala	Leu	450	455	460
Ile	Ile	Gln	Leu	Asn	Asn	Glu	Gly	Ile	Gln	Thr	Phe	Phe	Glu	Thr	Phe	465	470	475
Phe	Arg	Leu	Pro	Lys	Trp	Met	Trp	Arg	Gly	Phe	Leu	Gly	Ser	Thr	Leu	485	490	495

Ser Ser Val Asp Leu Ile Leu Phe Ala Phe Tyr Met Phe Thr Ile Ala
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 Pro Asn Gln Met Arg Met Asn Leu Val Arg His Leu Leu Ser Asp Pro
 515 520 525
 Thr Gly Ser Thr Met Ile Lys Thr Tyr Leu Thr Leu
 530 535 540

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 motif for epsilon-cyclase

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 <223> G/C variation

<220>
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 <222> (8)
 <223> A/S variation

<220>
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 <223> V/L variation

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 motif for epsilon-cyclase

<220>
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<220>
 <221> VARIANT
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<220>
 <221> VARIANT
 <222> (7)

<223> K/R variation

<220>

<221> VARIANT

<222> (8)

<223> V/L variation

<400> 18

Leu Asn Arg Xaa Tyr Gly Lys Val
1 5

<210> 19

<211> 8

<212> PRT

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motif for epsilon-cyclase

<220>

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1 5

<210> 20

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<212> PRT

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<220>

<221> VARIANT

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<223> P/A variation

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Pro Thr Phe Leu Tyr Ala Met Pro
1 5

<210> 21

<211> 14

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 motif for epsilon-cyclase

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 <223> M/S variation

 <220>
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 <222> (13)
 <223> A/V variation

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 Ala Xaa Met Val His Pro Ser Thr Gly Tyr Met Val Ala Arg
 1 5 10

 <210> 22
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 <213> Artificial sequence

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 motif for epsilon-cyclase

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      Met Glu Cys Phe Gly Ala Arg Asn Met Thr Ala Thr
      1          5          10
atg gcg gtt ttt acg tgc cct aga ttc acg gac tgt aat atc agg cac 160
Met Ala Val Phe Thr Cys Pro Arg Phe Thr Asp Cys Asn Ile Arg His
      15          20          25
aaa ttt tcg tta ctg aaa caa cga aga ttt act aat tta tca gca tcg 208
Lys Phe Ser Leu Leu Lys Gln Arg Arg Phe Thr Asn Leu Ser Ala Ser
      30          35          40
tct tcg ttg cgt caa att aag tgc agc gct aaa agc gac cgt tgt gta 256
Ser Ser Leu Arg Gln Ile Lys Cys Ser Ala Lys Ser Asp Arg Cys Val
      45          50          55          60
gtg gat aaa caa ggg att tcc gta gca gac gaa gaa gat tat gtg aag 304
Val Asp Lys Gln Gly Ile Ser Val Ala Asp Glu Glu Asp Tyr Val Lys
      65          70          75
gcc ggt gga tcg gag ctg ttt ttt gtt caa atg cag cgg act aag tcc 352
Ala Gly Gly Ser Glu Leu Phe Phe Val Gln Met Gln Arg Thr Lys Ser
      80          85          90
atg gaa agc cag tct aaa ctt tcc gaa aag cta gca cag ata cca att 400
Met Glu Ser Gln Ser Lys Leu Ser Glu Lys Leu Ala Gln Ile Pro Ile
      95          100          105
gga aat tgc ata ctt gat ctg gtt gta atc ggt tgt ggc cct gct ggc 448
Gly Asn Cys Ile Leu Asp Leu Val Val Ile Gly Cys Gly Pro Ala Gly
      110          115          120
ctt gct ctt gct gca gag tca gcc aaa cta ggg ttg aac gtt gga ctc 496
Leu Ala Leu Ala Ala Glu Ser Ala Lys Leu Gly Leu Asn Val Gly Leu
      125          130          135          140
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Ile Gly Pro Asp Leu Pro Phe Thr Asn Asn Tyr Gly Val Trp Gln Asp
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      160          165          170
gat act ctt gta tac ctt gat gat gct gat ccc atc cgc ata ggt cgt 640
Asp Thr Leu Val Tyr Leu Asp Asp Ala Asp Pro Ile Arg Ile Gly Arg
      175          180          185
gca tat ggc aga gtt cat cgt gat tta ctt cat gaa gag ttg tta aga 688
Ala Tyr Gly Arg Val His Arg Asp Leu Leu His Glu Glu Leu Leu Arg
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agg tgt gtg gaa tca ggt gtt tca tat cta agc tcc aaa gta gaa aga 736
Arg Cys Val Glu Ser Gly Val Ser Tyr Leu Ser Ser Lys Val Glu Arg
      205          210          215          220
atc act gaa gct cca aat ggc tat agt ctc att gaa tgt gaa ggc aat 784
Ile Thr Glu Ala Pro Asn Gly Tyr Ser Leu Ile Glu Cys Glu Gly Asn
      225          230          235
atc acc att cca tgc agg ctt gct act gtt gca tca ggg gca gct tca 832
Ile Thr Ile Pro Cys Arg Leu Ala Thr Val Ala Ser Gly Ala Ala Ser
      240          245          250
ggg aaa ttt ctg gag tat gaa ctt ggg ggt ccc cgt gtt tgt gtc caa 880
Gly Lys Phe Leu Glu Tyr Glu Leu Gly Gly Pro Arg Val Cys Val Gln
      255          260          265
aca gct tat ggt ata gag gtt gag gtt gaa aac aac ccc tat gat cca 928
Thr Ala Tyr Gly Ile Glu Val Glu Val Glu Asn Asn Pro Tyr Asp Pro
      270          275          280
gat cta atg gtg ttc atg gat tat aga gac ttc tca aaa cat aaa ccg 976
Asp Leu Met Val Phe Met Asp Tyr Arg Asp Phe Ser Lys His Lys Pro
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gaa tct tta gaa gca aaa tat ccg act ttc ctc tat gtc atg gcc atg 1024
Glu Ser Leu Glu Ala Lys Tyr Pro Thr Phe Leu Tyr Val Met Ala Met

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Ala Met Pro Phe Asn Leu Leu Lys Ser Lys Leu Met Ser Arg Leu Lys
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Ala Met Gly Ile Arg Ile Thr Arg Thr Tyr Glu Glu Glu Trp Ser Tyr
          350          355          360
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Ile Pro Val Gly Gly Ser Leu Pro Asn Thr Glu Gln Lys Asn Leu Ala
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Val Arg Ser Leu Ser Glu Ala Pro Asn Tyr Ala Ala Val Ile Ala Lys
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act aac att tca aaa caa gca tgg gaa aca ttg tgg cca ctt gaa agg 1408
Thr Asn Ile Ser Lys Gln Ala Trp Glu Thr Leu Trp Pro Leu Glu Arg
          430          435          440
aaa aga cag cga gcc ttc ttt cta ttc gga cta tca cac atc gtg cta 1456
Lys Arg Gln Arg Ala Phe Phe Leu Phe Gly Leu Ser His Ile Val Leu
          445          450          455          460
atg gat cta gag gga aca cgt aca ttt ttc cgt act ttc ttt cgt ttg 1504
Met Asp Leu Glu Gly Thr Arg Thr Phe Phe Arg Thr Phe Phe Arg Leu
          465          470          475
ccc aaa tgg atg tgg tgg gga ttt ttg ggg tct tct tta tct tca acg 1552
Pro Lys Trp Met Trp Trp Gly Phe Leu Gly Ser Ser Leu Ser Ser Thr
          480          485          490
gat ttg ata ata ttt gcg ctt tat atg ttt gtg ata gca cct cac agc 1600
Asp Leu Ile Ile Phe Ala Leu Tyr Met Phe Val Ile Ala Pro His Ser
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ttg aga atg gaa ctg gtt aga cat cta ctt tct gat ccg aca ggg gca 1648
Leu Arg Met Glu Leu Val Arg His Leu Leu Ser Asp Pro Thr Gly Ala
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act atg gta aaa gca tat ctc act ata tagatttaga ttatataaat 1695
Thr Met Val Lys Ala Tyr Leu Thr Ile
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<210> 24

<211> 533

<212> PRT

<213> Lactuca sativa

<400> 24

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Leu Lys Gln Arg Arg Phe Thr Asn Leu Ser Ala Ser Ser Ser Leu Arg
          35          40          45

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Glu	Leu	Phe	Phe	Val	Gln	Met	Gln	Arg	Thr	Lys	Ser	Met	Glu	Ser	Gln
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Ser	Lys	Leu	Ser	Glu	Lys	Leu	Ala	Gln	Ile	Pro	Ile	Gly	Asn	Cys	Ile
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Leu	Asp	Leu	Val	Val	Ile	Gly	Cys	Gly	Pro	Ala	Gly	Leu	Ala	Leu	Ala
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Ala	Glu	Ser	Ala	Lys	Leu	Gly	Leu	Asn	Val	Gly	Leu	Ile	Gly	Pro	Asp
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Leu	Pro	Phe	Thr	Asn	Asn	Tyr	Gly	Val	Trp	Gln	Asp	Glu	Phe	Ile	Gly
145					150					155					160
Leu	Gly	Leu	Glu	Gly	Cys	Ile	Glu	His	Ser	Trp	Lys	Asp	Thr	Leu	Val
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Tyr	Leu	Asp	Asp	Ala	Asp	Pro	Ile	Arg	Ile	Gly	Arg	Ala	Tyr	Gly	Arg
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Val	His	Arg	Asp	Leu	Leu	His	Glu	Leu	Leu	Arg	Arg	Cys	Val	Glu	
			195				200					205			
Ser	Gly	Val	Ser	Tyr	Leu	Ser	Ser	Lys	Val	Glu	Arg	Ile	Thr	Glu	Ala
						215						220			
Pro	Asn	Gly	Tyr	Ser	Leu	Ile	Glu	Cys	Glu	Gly	Asn	Ile	Thr	Ile	Pro
225					230					235					240
Cys	Arg	Leu	Ala	Thr	Val	Ala	Ser	Gly	Ala	Ala	Ser	Gly	Lys	Phe	Leu
				245					250					255	
Glu	Tyr	Glu	Leu	Gly	Gly	Pro	Arg	Val	Cys	Val	Gln	Thr	Ala	Tyr	Gly
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Ile	Glu	Val	Glu	Val	Glu	Asn	Asn	Pro	Tyr	Asp	Pro	Asp	Leu	Met	Val
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Phe	Met	Asp	Tyr	Arg	Asp	Phe	Ser	Lys	His	Lys	Pro	Glu	Ser	Leu	Glu
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Ala	Lys	Tyr	Pro	Thr	Phe	Leu	Tyr	Val	Met	Ala	Met	Ser	Pro	Thr	Lys
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Ile	Phe	Phe	Glu	Glu	Thr	Cys	Leu	Ala	Ser	Arg	Glu	Ala	Met	Pro	Phe
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Asn	Leu	Leu	Lys	Ser	Lys	Leu	Met	Ser	Arg	Leu	Lys	Ala	Met	Gly	Ile
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Arg	Ile	Thr	Arg	Thr	Tyr	Glu	Glu	Glu	Trp	Ser	Tyr	Ile	Pro	Val	Gly
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Gly	Ser	Leu	Pro	Asn	Thr	Glu	Gln	Lys	Asn	Leu	Ala	Phe	Gly	Ala	Ala
			370			375					380				
Ala	Ser	Met	Val	His	Pro	Ala	Thr	Gly	Tyr	Ser	Val	Val	Arg	Ser	Leu
385					390					395					400
Ser	Glu	Ala	Pro	Asn	Tyr	Ala	Ala	Val	Ile	Ala	Lys	Ile	Leu	Arg	Gln
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Lys	Gln	Ala	Trp	Glu	Thr	Leu	Trp	Pro	Leu	Glu	Arg	Lys	Arg	Gln	Arg
			435					440					445		
Ala	Phe	Phe	Leu	Phe	Gly	Leu	Ser	His	Ile	Val	Leu	Met	Asp	Leu	Glu
			450			455					460				
Gly	Thr	Arg	Thr	Phe	Phe	Arg	Thr	Phe	Phe	Arg	Leu	Pro	Lys	Trp	Met
465					470					475					480
Trp	Trp	Gly	Phe	Leu	Gly	Ser	Ser	Leu	Ser	Ser	Thr	Asp	Leu	Ile	Ile
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Phe	Ala	Leu	Tyr	Met	Phe	Val	Ile	Ala	Pro	His	Ser	Leu	Arg	Met	Glu
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Leu	Val	Arg	His	Leu	Leu	Ser	Asp	Pro	Thr	Gly	Ala	Thr	Met	Val	Lys
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Ala Tyr Leu Thr Ile
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<212> DNA
<213> Adonis palaestina

<220>
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<222> (116)..(1702)
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Met
1
gaa cta ctt ggt gtt cgc aac ctc atc tct tct tgc cct gtc tgg act 166
Glu Leu Leu Gly Val Arg Asn Leu Ile Ser Ser Cys Pro Val Trp Thr
5 10 15
ttt gga aca aga aac ctt agt agt tca aaa cta gct tat aac ata cat 214
Phe Gly Thr Arg Asn Leu Ser Ser Ser Lys Leu Ala Tyr Asn Ile His
20 25 30
cga tat ggt tct tct tgt aga gta gat ttt caa gtg agg gct gat ggt 262
Arg Tyr Gly Ser Ser Cys Arg Val Asp Phe Gln Val Arg Ala Asp Gly
35 40 45
gga agc ggg agt aga act tct gtt gct tat aaa gag ggt ttt gtg gac 310
Gly Ser Gly Ser Arg Thr Ser Val Ala Tyr Lys Glu Gly Phe Val Asp
50 55 60 65
gag gag gat ttt atc aaa gct ggt ggt tct gag ctt ttg ttt gtc caa 358
Glu Glu Asp Phe Ile Lys Ala Gly Gly Ser Glu Leu Leu Phe Val Gln
70 75 80
atg cag caa aca aag tct atg gag aaa cag gcc aag ctc gcc gat aag 406
Met Gln Gln Thr Lys Ser Met Glu Lys Gln Ala Lys Leu Ala Asp Lys
85 90 95
ttg cca cca ata cct ttc gga gaa tct gtg atg gac ttg gtt gta ata 454
Leu Pro Pro Ile Pro Phe Gly Glu Ser Val Met Asp Leu Val Val Ile
100 105 110
ggt tgt gga cct gct ggt ctt tca ctg gct gca gaa gct gct aag cta 502
Gly Cys Gly Pro Ala Gly Leu Ser Leu Ala Ala Glu Ala Ala Lys Leu
115 120 125
ggc ttg aaa gtt ggc ctt att ggt cct gat ctt cct ttt aca aat aat 550
Gly Leu Lys Val Gly Leu Ile Gly Pro Asp Leu Pro Phe Thr Asn Asn
130 135 140 145
tat ggt gtg tgg gaa gac gag ttc aaa gat ctt gga ctt gaa cgt tgt 598
Tyr Gly Val Trp Glu Asp Glu Phe Lys Asp Leu Gly Leu Glu Arg Cys
150 155 160
atc gag cat gct tgg aag gac acc atc gta tat ctt gac aat gat gct 646
Ile Glu His Ala Trp Lys Asp Thr Ile Val Tyr Leu Asp Asn Asp Ala
165 170 175
cct gtc ctt att ggt cgt gca tat gga cga gtt agc cgg cat ttg ctg 694
Pro Val Leu Ile Gly Arg Ala Tyr Gly Arg Val Ser Arg His Leu Leu
180 185 190
cat gaa gag ttg ctg aaa agg tgt gtc gag tca ggt gta tca tat ctg 742
His Glu Glu Leu Leu Lys Arg Cys Val Glu Ser Gly Val Ser Tyr Leu
195 200 205
aat tct aaa gtg gaa agg atc act gaa gct ggt gat ggc cat agt ctt 790

Asn 210	Ser	Lys	Val	Glu	Arg 215	Ile	Thr	Glu	Ala	Gly 220	Asp	Gly	His	Ser	Leu 225	
gta	ggt	tgt	gaa	aac	gac	atc	ttt	atc	cct	tgc	agg	ctt	gct	act	ggt	838
Val	Val	Cys	Glu	Asn	Asp	Ile	Phe	Ile	Pro	Cys	Arg	Leu	Ala	Thr	Val	
				230					235						240	
gca	tct	gga	gca	gct	tca	ggg	aaa	ctt	ttg	gag	tat	gaa	gta	ggg	ggc	886
Ala	Ser	Gly	Ala	Ala	Ser	Gly	Lys	Leu	Leu	Glu	Tyr	Glu	Val	Gly	Gly	
				245					250						255	
cct	cgt	ggt	tgt	gtc	caa	act	gct	tat	ggg	gtg	gag	ggt	gag	gtg	gag	934
Pro	Arg	Val	Cys	Val	Gln	Thr	Ala	Tyr	Gly	Val	Glu	Val	Glu	Val	Glu	
				260					265						270	
aac	aat	cca	tac	gat	ccc	aac	tta	atg	gta	ttt	atg	gac	tac	aga	gac	982
Asn	Asn	Pro	Tyr	Asp	Pro	Asn	Leu	Met	Val	Phe	Met	Asp	Tyr	Arg	Asp	
				275												
tat	atg	caa	cag	aaa	tta	cag	tgc	tcg	gaa	gaa	gaa	tat	cca	aca	ttt	1030
Tyr	Met	Gln	Gln	Lys	Leu	Gln	Cys	Ser	Glu	Glu	Glu	Tyr	Pro	Thr	Phe	
				290												
ctc	tat	gtc	atg	ccc	atg	tcg	cca	aca	aga	ctt	ttt	ttt	gag	gaa	acc	1078
Leu	Tyr	Val	Met	Pro	Met	Ser	Pro	Thr	Arg	Leu	Phe	Phe	Glu	Glu	Thr	
				310												
tgt	ttg	gcc	tca	aaa	gat	gcc	atg	cct	ttc	gat	cta	ctg	aag	aga	aaa	1126
Cys	Leu	Ala	Ser	Lys	Asp	Ala	Met	Pro	Phe	Asp	Leu	Leu	Lys	Arg	Lys	
				325												
cta	atg	tca	cga	ttg	aag	act	ctg	ggg	atc	caa	ggt	aca	aaa	att	tat	1174
Leu	Met	Ser	Arg	Leu	Lys	Thr	Leu	Gly	Ile	Gln	Val	Thr	Lys	Ile	Tyr	
				340												
gaa	gag	gaa	tgg	tct	tat	att	cct	ggt	ggg	ggg	tct	tta	cca	aac	aca	1222
Glu	Glu	Glu	Trp	Ser	Tyr	Ile	Pro	Val	Gly	Gly	Ser	Leu	Pro	Asn	Thr	
				355												
gag	caa	aag	aac	cta	gca	ttt	ggg	gct	gca	gca	agc	atg	gtg	cat	cca	1270
Glu	Gln	Lys	Asn	Leu	Ala	Phe	Gly	Ala	Ala	Ala	Ser	Met	Val	His	Pro	
				370												
gca	aca	ggc	tat	tcg	ggt	gta	cga	tca	cta	tca	gaa	gct	cca	aaa	tat	1318
Ala	Thr	Gly	Tyr	Ser	Val	Val	Arg	Ser	Leu	Ser	Glu	Ala	Pro	Lys	Tyr	
				390												
gct	tct	gta	att	gca	aag	att	ttg	aag								

tatgatcatc tctatgtata tcctatatcc taatctcata aagtaatcga aaattcattg 1822
 atagaaaaaa aaaaaaaaaa aaaaaa 1848

<210> 26
 <211> 529
 <212> PRT
 <213> Adonis palaestina

<400> 26
 Met Glu Leu Leu Gly Val Arg Asn Leu Ile Ser Ser Cys Pro Val Trp
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 Thr Phe Gly Thr Arg Asn Leu Ser Ser Ser Lys Leu Ala Tyr Asn Ile
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 His Arg Tyr Gly Ser Ser Cys Arg Val Asp Phe Gln Val Arg Ala Asp
 35 40 45
 Gly Gly Ser Gly Ser Arg Thr Ser Val Ala Tyr Lys Glu Gly Phe Val
 50 55 60
 Asp Glu Glu Asp Phe Ile Lys Ala Gly Gly Ser Glu Leu Leu Phe Val
 65 70 75 80
 Gln Met Gln Gln Thr Lys Ser Met Glu Lys Gln Ala Lys Leu Ala Asp
 85 90 95
 Lys Leu Pro Pro Ile Pro Phe Gly Glu Ser Val Met Asp Leu Val Val
 100 105 110
 Ile Gly Cys Gly Pro Ala Gly Leu Ser Leu Ala Ala Glu Ala Ala Lys
 115 120 125
 Leu Gly Leu Lys Val Gly Leu Ile Gly Pro Asp Leu Pro Phe Thr Asn
 130 135 140
 Asn Tyr Gly Val Trp Glu Asp Glu Phe Lys Asp Leu Gly Leu Glu Arg
 145 150 155 160
 Cys Ile Glu His Ala Trp Lys Asp Thr Ile Val Tyr Leu Asp Asn Asp
 165 170 175
 Ala Pro Val Leu Ile Gly Arg Ala Tyr Gly Arg Val Ser Arg His Leu
 180 185 190
 Leu His Glu Glu Leu Leu Lys Arg Cys Val Glu Ser Gly Val Ser Tyr
 195 200 205
 Leu Asn Ser Lys Val Glu Arg Ile Thr Glu Ala Gly Asp Gly His Ser
 210 215 220
 Leu Val Val Cys Glu Asn Asp Ile Phe Ile Pro Cys Arg Leu Ala Thr
 225 230 235 240
 Val Ala Ser Gly Ala Ala Ser Gly Lys Leu Leu Glu Tyr Glu Val Gly
 245 250 255
 Gly Pro Arg Val Cys Val Gln Thr Ala Tyr Gly Val Glu Val Glu Val
 260 265 270
 Glu Asn Asn Pro Tyr Asp Pro Asn Leu Met Val Phe Met Asp Tyr Arg
 275 280 285
 Asp Tyr Met Gln Gln Lys Leu Gln Cys Ser Glu Glu Glu Tyr Pro Thr
 290 295 300
 Phe Leu Tyr Val Met Pro Met Ser Pro Thr Arg Leu Phe Phe Glu Glu
 305 310 315 320
 Thr Cys Leu Ala Ser Lys Asp Ala Met Pro Phe Asp Leu Leu Lys Arg
 325 330 335
 Lys Leu Met Ser Arg Leu Lys Thr Leu Gly Ile Gln Val Thr Lys Ile
 340 345 350
 Tyr Glu Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser Leu Pro Asn
 355 360 365
 Thr Glu Gln Lys Asn Leu Ala Phe Gly Ala Ala Ala Ser Met Val His
 370 375 380
 Pro Ala Thr Gly Tyr Ser Val Val Arg Ser Leu Ser Glu Ala Pro Lys

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385          390          395          400
Tyr Ala Ser Val Ile Ala Lys Ile Leu Lys Gln Asp Asn Ser Ala Tyr
          405          410          415
Val Val Ser Gly Gln Ser Ser Ala Val Asn Ile Ser Met Gln Ala Trp
          420          425          430
Ser Ser Leu Trp Pro Lys Glu Arg Lys Arg Gln Arg Ala Phe Phe Leu
          435          440          445
Phe Gly Leu Glu Leu Ile Val Gln Leu Asp Ile Glu Ala Thr Arg Thr
          450          455          460
Phe Phe Arg Thr Phe Phe Arg Leu Pro Thr Trp Met Trp Trp Gly Phe
465          470          475          480
Leu Gly Ser Ser Leu Ser Ser Phe Asp Leu Val Leu Phe Ser Met Tyr
          485          490          495
Met Phe Val Leu Ala Pro Asn Ser Met Arg Met Ser Leu Val Arg His
          500          505          510
Leu Leu Ser Asp Pro Ser Gly Ala Val Met Val Lys Ala Tyr Leu Glu
          515          520          525
Arg

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<210> 27
<211> 1898
<212> DNA
<213> Adonis palaestina

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<220>
<221> CDS
<222> (113)..(1699)
<223> coding for epsilon-cyclase

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<400> 27
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tttcttcttt tctcttcaaa acaacaaact aatgtgagca gagtatctgg ct atg gaa 118
                                     Met Glu
                                     1
cta ctt ggt gtt cgc aac ctc atc tct tct tgc cct gtg tgg act ttt 166
Leu Leu Gly Val Arg Asn Leu Ile Ser Ser Cys Pro Val Trp Thr Phe
          5          10          15
gga aca aga aac ctt agt agt tca aaa cta gct tat aac ata cat cga 214
Gly Thr Arg Asn Leu Ser Ser Ser Lys Leu Ala Tyr Asn Ile His Arg
          20          25          30
tat ggt tct tct tgt aga gta gat ttt caa gtg aga gct gat ggt gga 262
Tyr Gly Ser Ser Cys Arg Val Asp Phe Gln Val Arg Ala Asp Gly Gly
          35          40          45          50
agc ggg agt aga agt tct gtt gct tat aaa gag ggt ttt gtg gat gaa 310
Ser Gly Ser Arg Ser Ser Val Ala Tyr Lys Glu Gly Phe Val Asp Glu
          55          60          65
gag gat ttt atc aaa gct ggt ggt tct gag ctt ttg ttt gtc caa atg 358
Glu Asp Phe Ile Lys Ala Gly Gly Ser Glu Leu Leu Phe Val Gln Met
          70          75          80
cag caa aca aag tct atg gag aaa cag gcc aag ctc gcc gat aag ttg 406
Gln Gln Thr Lys Ser Met Glu Lys Gln Ala Lys Leu Ala Asp Lys Leu
          85          90          95
cca cca ata cct ttt gga gaa tcc gtg atg gac ttg gtt gta ata ggt 454
Pro Pro Ile Pro Phe Gly Glu Ser Val Met Asp Leu Val Val Ile Gly
          100          105          110
tgt gga cct gct ggt ctt tca ctg gct gca gaa gct gct aag cta ggg 502
Cys Gly Pro Ala Gly Leu Ser Leu Ala Ala Glu Ala Ala Lys Leu Gly
115          120          125          130

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ttg	aaa	ggt	ggc	ctt	att	ggt	cct	gat	ctt	cct	ttt	aca	aat	aat	tat	550
Leu	Lys	Val	Gly	Leu	Ile	Gly	Pro	Asp	Leu	Pro	Phe	Thr	Asn	Asn	Tyr	
			135						140						145	
ggt	gtg	tgg	gaa	gac	gag	ttc	aaa	gat	ctt	gga	ctt	gaa	cgt	tgt	atc	598
Gly	Val	Trp	Glu	Asp	Glu	Phe	Lys	Asp	Leu	Gly	Leu	Glu	Arg	Cys	Ile	
			150					155						160		
gag	cat	gct	tgg	aag	gac	acc	atc	gta	tat	ctt	gat	aat	gat	gct	cct	646
Glu	His	Ala	Trp	Lys	Asp	Thr	Ile	Val	Tyr	Leu	Asp	Asn	Asp	Ala	Pro	
			165				170							175		
gtc	ctt	att	ggt	cgt	gca	tat	gga	cga	ggt	agt	cga	cat	ttg	cta	cat	694
Val	Leu	Ile	Gly	Arg	Ala	Tyr	Gly	Arg	Val	Ser	Arg	His	Leu	Leu	His	
	180					185					190					
gag	gag	ttg	ctg	aaa	agg	tgt	gtg	gag	tca	ggt	gta	tca	tat	ctg	gat	742
Glu	Glu	Leu	Leu	Lys	Arg	Cys	Val	Glu	Ser	Gly	Val	Ser	Tyr	Leu	Asp	
195					200					205					210	
tct	aaa	gtg	gaa	agg	atc	act	gaa	gct	ggt	gat	ggc	cat	agc	ctt	gta	790
Ser	Lys	Val	Glu	Arg	Ile	Thr	Glu	Ala	Gly	Asp	Gly	His	Ser	Leu	Val	
				215					220					225		
ggt	tgt	gaa	aat	gag	atc	ttt	atc	cct	tgc	agg	ctt	gct	act	ggt	gca	838
Val	Cys	Glu	Asn	Glu	Ile	Phe	Ile	Pro	Cys	Arg	Leu	Ala	Thr	Val	Ala	
			230					235						240		
tct	gga	gca	gct	tca	ggg	aaa	ctt	ttg	gag	tat	gaa	gta	ggt	ggc	cct	886
Ser	Gly	Ala	Ala	Ser	Gly	Lys	Leu	Leu	Glu	Tyr	Glu	Val	Gly	Gly	Pro	
	245					250						255				
cgt	ggt	tgt	gtc	caa	acc	gct	tat	ggg	gtg	gag	ggt	gag	gtg	gag	aac	934
Arg	Val	Cys	Val	Gln	Thr	Ala	Tyr	Gly	Val	Glu	Val	Glu	Val	Glu	Asn	
	260					265					270					
aat	cca	tac	gat	ccc	aac	tta	atg	gta	ttc	atg	gac	tac	aga	gac	tat	982
Asn	Pro	Tyr	Asp	Pro	Asn	Leu	Met	Val	Phe	Met	Asp	Tyr	Arg	Asp	Tyr	
275					280					285					290	
atg	caa	cag	aaa	tta	cag	tgc	tcg	gaa	gaa	gaa	tat	cca	aca	ttt	ctc	1030
Met	Gln	Gln	Lys	Leu	Gln	Cys	Ser	Glu	Glu	Glu	Tyr	Pro	Thr	Phe	Leu	
				295					300					305		
tat	gtc	atg	ccc	atg	tcg	cca	aca	aga	ctt	ttt	ttt	gag	gaa	acc	tgt	1078
Tyr	Val	Met	Pro	Met	Ser	Pro	Thr	Arg	Leu	Phe	Phe	Glu	Glu	Thr	Cys	
			310					315						320		
ttg	gcc	tca	aaa	gat	gcc	atg	cca	ttc	gat	cta	ctg	aag	aga	aaa	ctg	1126
Leu	Ala	Ser	Lys	Asp	Ala	Met	Pro	Phe	Asp	Leu	Leu	Lys	Arg	Lys	Leu	
			325				330							335		
atg	tca	cga	ttg	aag	act	ctg	ggt	atc	caa	ggt	aca	aaa	ggt	tat	gaa	1174
Met	Ser	Arg	Leu	Lys	Thr	Leu	Gly	Ile	Gln	Val	Thr	Lys	Val	Tyr	Glu	
	340					345					350					
gag	gaa	tgg	tca	tat	att	cct	ggt	ggt	ggt	tct	tta	cca	aac	aca	gag	1222
Glu	Glu	Trp	Ser	Tyr	Ile	Pro	Val	Gly	Gly	Ser	Leu	Pro	Asn	Thr	Glu	
355					360					365					370	
caa	aag	aac	cta	gca	ttt	ggt	gct	gca	gca	agc	atg	gtg	cat	cca	gca	1270
Gln	Lys	Asn	Leu	Ala	Phe	Gly	Ala	Ala	Ala	Ser	Met	Val	His	Pro	Ala	
				375					380					385		
aca	ggc	tat	tcg	ggt	gta	cgg	tca	ctg	tca	gaa	gct	cca	aaa	tat	gct	1318
Thr	Gly	Tyr	Ser	Val	Val	Arg	Ser	Leu	Ser	Glu	Ala	Pro	Lys	Tyr	Ala	
			390					395						400		
tct	gta	att	gca	aag	att	ttg	aag	caa	gat	aac	tct	gcg	tat	gtg	ggt	1366
Ser	Val	Ile	Ala	Lys	Ile	Leu	Lys	Gln	Asp	Asn	Ser	Ala	Tyr	Val	Val	
	405					410								415		
tct	gga	caa	agt	agt	gca	gta	aac	att	tca	atg	caa	gca	tgg	agc	agt	1414
Ser	Gly	Gln	Ser	Ser	Ala	Val	Asn	Ile	Ser	Met	Gln	Ala	Trp	Ser	Ser	
	420					425						430				
ctt	tgg	cca	aag	gag	cga	aaa	cgt	caa	aga	gca	ttc	ttt	ctt	ttt	gga	1462
Leu	Trp	Pro	Lys	Glu	Arg	Lys	Arg	Gln	Arg	Ala	Phe	Phe	Leu	Phe	Gly	
435					440					445					450	

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tta gag ctt att gtg cag cta gat att gaa gca acc aga aca ttc ttt 1510
Leu Glu Leu Ile Val Gln Leu Asp Ile Glu Ala Thr Arg Thr Phe Phe
      455                                460                                465
aga acc ttc ttc cgc ttg cca act tgg atg tgg tgg ggt ttc ctt ggg 1558
Arg Thr Phe Phe Arg Leu Pro Thr Trp Met Trp Trp Gly Phe Leu Gly
      470                                475                                480
tct tca cta tca tct ttc gat ctc gtc ttg ttt tcc atg tac atg ttt 1606
Ser Ser Leu Ser Ser Phe Asp Leu Val Leu Phe Ser Met Tyr Met Phe
      485                                490                                495
gtt ttg gcg cca aac agc atg agg atg tca ctt gtg aga cat ttg ctt 1654
Val Leu Ala Pro Asn Ser Met Arg Met Ser Leu Val Arg His Leu Leu
      500                                505                                510
tca gat cct tct ggt gca gtt atg gta aga gct tac ctc gaa agg 1699
Ser Asp Pro Ser Gly Ala Val Met Val Arg Ala Tyr Leu Glu Arg
      515                                520                                525
tagtctcatc tattattaaa ctctagtgtt tcaccaaata aatgaggatc cttcgaatgt 1759
gtatatgatc atctctatgt atatcctgta ctctaattctc ataaagtata tgccggggtt 1819
gatattgttg tgtcaaaccg gccaatgata taaagtaaat ttattgatac aaaagtagtt 1879
tttttcctta aaaaaaaaaa 1898

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<210> 28
 <211> 529
 <212> PRT
 <213> Adonis palaestina

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<400> 28
Met Glu Leu Leu Gly Val Arg Asn Leu Ile Ser Ser Cys Pro Val Trp
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Thr Phe Gly Thr Arg Asn Leu Ser Ser Ser Lys Leu Ala Tyr Asn Ile
      20      25      30
His Arg Tyr Gly Ser Ser Cys Arg Val Asp Phe Gln Val Arg Ala Asp
      35      40      45
Gly Gly Ser Gly Ser Arg Ser Ser Val Ala Tyr Lys Glu Gly Phe Val
      50      55      60
Asp Glu Glu Asp Phe Ile Lys Ala Gly Gly Ser Glu Leu Leu Phe Val
      65      70      75      80
Gln Met Gln Gln Thr Lys Ser Met Glu Lys Gln Ala Lys Leu Ala Asp
      85      90      95
Lys Leu Pro Pro Ile Pro Phe Gly Glu Ser Val Met Asp Leu Val Val
      100     105     110
Ile Gly Cys Gly Pro Ala Gly Leu Ser Leu Ala Ala Glu Ala Ala Lys
      115     120     125
Leu Gly Leu Lys Val Gly Leu Ile Gly Pro Asp Leu Pro Phe Thr Asn
      130     135     140
Asn Tyr Gly Val Trp Glu Asp Glu Phe Lys Asp Leu Gly Leu Glu Arg
      145     150     155     160
Cys Ile Glu His Ala Trp Lys Asp Thr Ile Val Tyr Leu Asp Asn Asp
      165     170     175
Ala Pro Val Leu Ile Gly Arg Ala Tyr Gly Arg Val Ser Arg His Leu
      180     185     190
Leu His Glu Leu Leu Lys Arg Cys Val Glu Ser Gly Val Ser Tyr
      195     200     205
Leu Asp Ser Lys Val Glu Arg Ile Thr Glu Ala Gly Asp Gly His Ser
      210     215     220
Leu Val Val Cys Glu Asn Glu Ile Phe Ile Pro Cys Arg Leu Ala Thr
      225     230     235     240
Val Ala Ser Gly Ala Ala Ser Gly Lys Leu Leu Glu Tyr Glu Val Gly
      245     250     255

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Gly Pro Arg Val Cys Val Gln Thr Ala Tyr Gly Val Glu Val Glu Val
 260 265 270
 Glu Asn Asn Pro Tyr Asp Pro Asn Leu Met Val Phe Met Asp Tyr Arg
 275 280 285
 Asp Tyr Met Gln Gln Lys Leu Gln Cys Ser Glu Glu Glu Tyr Pro Thr
 290 295 300
 Phe Leu Tyr Val Met Pro Met Ser Pro Thr Arg Leu Phe Phe Glu Glu
 305 310 315 320
 Thr Cys Leu Ala Ser Lys Asp Ala Met Pro Phe Asp Leu Leu Lys Arg
 325 330 335
 Lys Leu Met Ser Arg Leu Lys Thr Leu Gly Ile Gln Val Thr Lys Val
 340 345 350
 Tyr Glu Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser Leu Pro Asn
 355 360 365
 Thr Glu Gln Lys Asn Leu Ala Phe Gly Ala Ala Ala Ser Met Val His
 370 375 380
 Pro Ala Thr Gly Tyr Ser Val Val Arg Ser Leu Ser Glu Ala Pro Lys
 385 390 395 400
 Tyr Ala Ser Val Ile Ala Lys Ile Leu Lys Gln Asp Asn Ser Ala Tyr
 405 410 415
 Val Val Ser Gly Gln Ser Ser Ala Val Asn Ile Ser Met Gln Ala Trp
 420 425 430
 Ser Ser Leu Trp Pro Lys Glu Arg Lys Arg Gln Arg Ala Phe Phe Leu
 435 440 445
 Phe Gly Leu Glu Leu Ile Val Gln Leu Asp Ile Glu Ala Thr Arg Thr
 450 455 460
 Phe Phe Arg Thr Phe Phe Arg Leu Pro Thr Trp Met Trp Trp Gly Phe
 465 470 475 480
 Leu Gly Ser Ser Leu Ser Ser Phe Asp Leu Val Leu Phe Ser Met Tyr
 485 490 495
 Met Phe Val Leu Ala Pro Asn Ser Met Arg Met Ser Leu Val Arg His
 500 505 510
 Leu Leu Ser Asp Pro Ser Gly Ala Val Met Val Arg Ala Tyr Leu Glu
 515 520 525
 Arg

<210> 29

<211> 1661

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (2)..(1501)

<223> coding for epsilon-cyclase

<400> 29

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 1 5 10 15
 cag ttt cat ggg ttt gag aga tta tgc agt aac aat cca tac cct tca 97
 Gln Phe His Gly Phe Glu Arg Leu Cys Ser Asn Asn Pro Tyr Pro Ser
 20 25 30
 agg gtt agg ctt ggt gtg aag aaa agg gct atc aaa att gtc tct agt 145
 Arg Val Arg Leu Gly Val Lys Lys Arg Ala Ile Lys Ile Val Ser Ser
 35 40 45
 gta gtg agt ggt agc gct gct ctt ttg gat ctt gtt cct gaa act aag 193
 Val Val Ser Gly Ser Ala Ala Leu Leu Asp Leu Val Pro Glu Thr Lys

50	55	60	
aag gag aat ctt gac ttt gag ctt cct ttg tac gac act tcc aag agt	241		
Lys Glu Asn Leu Asp Phe Glu Leu Pro Leu Tyr Asp Thr Ser Lys Ser			
65 70 75 80			
caa gtt gtt gat ttg gct att gtt ggt ggt ggt cct gct ggt tta gcc	289		
Gln Val Val Asp Leu Ala Ile Val Gly Gly Gly Pro Ala Gly Leu Ala			
85 90 95			
gtg gct cag cag gtt tct gaa gct gga ctc tct gtt tgt tcc att gat	337		
Val Ala Gln Gln Val Ser Glu Ala Gly Leu Ser Val Cys Ser Ile Asp			
100 105 110			
cct tct cct aag ctc ata tgg cct aac aat tat gga gtt tgg gtt gat	385		
Pro Ser Pro Lys Leu Ile Trp Pro Asn Asn Tyr Gly Val Trp Val Asp			
115 120 125			
gag ttt gag gct atg gat tta cta gac tgc ctg gat acc aca tgg tct	433		
Glu Phe Glu Ala Met Asp Leu Leu Asp Cys Leu Asp Thr Thr Trp Ser			
130 135 140			
ggg gct gtt gtc tat gtc gat gaa ggt gtc aag aag gat ttg agc cgg	481		
Gly Ala Val Val Tyr Val Asp Glu Gly Val Lys Lys Asp Leu Ser Arg			
145 150 155 160			
cct tat ggg aga gtt aac cgg aaa cag ctc aaa tcc aaa atg ctt cag	529		
Pro Tyr Gly Arg Val Asn Arg Lys Gln Leu Lys Ser Lys Met Leu Gln			
165 170 175			
aaa tgt att acc aac ggt gtt aaa ttt cat cag tct aag gtc act aat	577		
Lys Cys Ile Thr Asn Gly Val Lys Phe His Gln Ser Lys Val Thr Asn			
180 185 190			
gtg gtt cac gag gag gca aac tcc act gtg gtc tgc agt gac ggt gta	625		
Val Val His Glu Glu Ala Asn Ser Thr Val Val Cys Ser Asp Gly Val			
195 200 205			
aag att cag gct tcc gtg gtt ctt gat gcc act ggg ttt tcc cga tgc	673		
Lys Ile Gln Ala Ser Val Val Leu Asp Ala Thr Gly Phe Ser Arg Cys			
210 215 220			
ttg gtt cag tat gac aaa cct tac aac cct ggg tac caa gta gct tac	721		
Leu Val Gln Tyr Asp Lys Pro Tyr Asn Pro Gly Tyr Gln Val Ala Tyr			
225 230 235 240			
ggg att ata gct gaa gtt gat ggt cac cca ttc gat gta gac aaa atg	769		
Gly Ile Ile Ala Glu Val Asp Gly His Pro Phe Asp Val Asp Lys Met			
245 250 255			
gtg ttc atg gat tgg aga gac aaa cat ctg gac tca tat cct gag ctg	817		
Val Phe Met Asp Trp Arg Asp Lys His Leu Asp Ser Tyr Pro Glu Leu			
260 265 270			
aaa gaa cgg aac agc aag atc cca acg ttc ttg tac gct atg cca ttt	865		
Lys Glu Arg Asn Ser Lys Ile Pro Thr Phe Leu Tyr Ala Met Pro Phe			
275 280 285			
tct tcc aac cga ata ttt ctt gaa gaa act tct tta gtt gct aga cct	913		
Ser Ser Asn Arg Ile Phe Leu Glu Glu Thr Ser Leu Val Ala Arg Pro			
290 295 300			
ggg ctg aga atg gaa gat atc caa gaa aga atg gct gct aga ctg aaa	961		
Gly Leu Arg Met Glu Asp Ile Gln Glu Arg Met Ala Ala Arg Leu Lys			
305 310 315 320			
cat ctg ggg atc aat gtg aag agg att gag gaa gac gag cgt tgt gtg	1009		
His Leu Gly Ile Asn Val Lys Arg Ile Glu Glu Asp Glu Arg Cys Val			
325 330 335			
atc ccg atg ggc ggt cct tta cca gtc tta cct caa cgg gtt gtg ggg	1057		
Ile Pro Met Gly Gly Pro Leu Pro Val Leu Pro Gln Arg Val Val Gly			
340 345 350			
att ggt ggg aca gca gga atg gtt cat cct tca act ggt tac atg gtt	1105		
Ile Gly Gly Thr Ala Gly Met Val His Pro Ser Thr Gly Tyr Met Val			
355 360 365			
gct agg act ctt gca gct gca cca ata gtt gca aat gcc att gtg aga	1153		
Ala Arg Thr Leu Ala Ala Ala Pro Ile Val Ala Asn Ala Ile Val Arg			

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      370      375      380
tac ctc ggt tca cca agt agt aat agc ctg aga gga gat caa ctc tct 1201
Tyr Leu Gly Ser Pro Ser Ser Asn Ser Leu Arg Gly Asp Gln Leu Ser
385      390      395      400
gct gag gtt tgg aga gac ttg tgg cct atc gaa cgg cgt aga cag agg 1249
Ala Glu Val Trp Arg Asp Leu Trp Pro Ile Glu Arg Arg Arg Gln Arg
      405      410      415
gag ttc ttc tgt ttt gga atg gat att ctg ctg aaa ctc gat tta gac 1297
Glu Phe Phe Cys Phe Gly Met Asp Ile Leu Leu Lys Leu Asp Leu Asp
      420      425      430
gct act aga agg ttc ttt gat gca ttc ttt gat ctg caa cct cat tac 1345
Ala Thr Arg Arg Phe Phe Asp Ala Phe Phe Asp Leu Gln Pro His Tyr
      435      440      445
tgg cac gga ttc ttg tct tcc agg ctg ttt ctc ccg gaa ctg ttg gtc 1393
Trp His Gly Phe Leu Ser Ser Arg Leu Phe Leu Pro Glu Leu Leu Val
      450      455      460
ttc ggg ttg tcg ctc ttc tca cac gct tcc aat acc tca aga ttg gag 1441
Phe Gly Leu Ser Leu Phe Ser His Ala Ser Asn Thr Ser Arg Leu Glu
465      470      475      480
atc atg aca aag ggg act gtt cct ctt gct aag atg atc aac aat ttg 1489
Ile Met Thr Lys Gly Thr Val Pro Leu Ala Lys Met Ile Asn Asn Leu
      485      490      495
gta caa gat aga gactaaggac cagaaactta gacatataag tataatctggt 1541
Val Gln Asp Arg
      500
ctttgggttct tgaccagtag tatatccgca ttgcaagtcg ttggataatt gtgtataaac 1601
cacagatcca taacctgaat ccttgtgaaa tcaaattggt actactagtt cattaaaacc 1661

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<210> 30
 <211> 500
 <212> PRT
 <213> Arabidopsis thaliana

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<400> 30
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Gln Phe His Gly Phe Glu Arg Leu Cys Ser Asn Asn Pro Tyr Pro Ser
      20      25      30
Arg Val Arg Leu Gly Val Lys Lys Arg Ala Ile Lys Ile Val Ser Ser
      35      40      45
Val Val Ser Gly Ser Ala Ala Leu Leu Asp Leu Val Pro Glu Thr Lys
      50      55      60
Lys Glu Asn Leu Asp Phe Glu Leu Pro Leu Tyr Asp Thr Ser Lys Ser
      65      70      75      80
Gln Val Val Asp Leu Ala Ile Val Gly Gly Gly Pro Ala Gly Leu Ala
      85      90      95
Val Ala Gln Gln Val Ser Glu Ala Gly Leu Ser Val Cys Ser Ile Asp
      100      105      110
Pro Ser Pro Lys Leu Ile Trp Pro Asn Asn Tyr Gly Val Trp Val Asp
      115      120      125
Glu Phe Glu Ala Met Asp Leu Leu Asp Cys Leu Asp Thr Thr Trp Ser
      130      135      140
Gly Ala Val Val Tyr Val Asp Glu Gly Val Lys Lys Asp Leu Ser Arg
      145      150      155      160
Pro Tyr Gly Arg Val Asn Arg Lys Gln Leu Lys Ser Lys Met Leu Gln
      165      170      175
Lys Cys Ile Thr Asn Gly Val Lys Phe His Gln Ser Lys Val Thr Asn
      180      185      190
Val Val His Glu Glu Ala Asn Ser Thr Val Val Cys Ser Asp Gly Val

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	195		200		205										
Lys	Ile	Gln	Ala	Ser	Val	Val	Leu	Asp	Ala	Thr	Gly	Phe	Ser	Arg	Cys
	210					215					220				
Leu	Val	Gln	Tyr	Asp	Lys	Pro	Tyr	Asn	Pro	Gly	Tyr	Gln	Val	Ala	Tyr
225					230					235					240
Gly	Ile	Ile	Ala	Glu	Val	Asp	Gly	His	Pro	Phe	Asp	Val	Asp	Lys	Met
			245					250						255	
Val	Phe	Met	Asp	Trp	Arg	Asp	Lys	His	Leu	Asp	Ser	Tyr	Pro	Glu	Leu
		260					265					270			
Lys	Glu	Arg	Asn	Ser	Lys	Ile	Pro	Thr	Phe	Leu	Tyr	Ala	Met	Pro	Phe
	275						280					285			
Ser	Ser	Asn	Arg	Ile	Phe	Leu	Glu	Glu	Thr	Ser	Leu	Val	Ala	Arg	Pro
	290					295					300				
Gly	Leu	Arg	Met	Glu	Asp	Ile	Gln	Glu	Arg	Met	Ala	Ala	Arg	Leu	Lys
305					310					315					320
His	Leu	Gly	Ile	Asn	Val	Lys	Arg	Ile	Glu	Glu	Asp	Glu	Arg	Cys	Val
			325						330					335	
Ile	Pro	Met	Gly	Gly	Pro	Leu	Pro	Val	Leu	Pro	Gln	Arg	Val	Val	Gly
		340						345					350		
Ile	Gly	Gly	Thr	Ala	Gly	Met	Val	His	Pro	Ser	Thr	Gly	Tyr	Met	Val
	355						360					365			
Ala	Arg	Thr	Leu	Ala	Ala	Ala	Pro	Ile	Val	Ala	Asn	Ala	Ile	Val	Arg
	370					375					380				
Tyr	Leu	Gly	Ser	Pro	Ser	Ser	Asn	Ser	Leu	Arg	Gly	Asp	Gln	Leu	Ser
385					390					395					400
Ala	Glu	Val	Trp	Arg	Asp	Leu	Trp	Pro	Ile	Glu	Arg	Arg	Arg	Gln	Arg
			405					410						415	
Glu	Phe	Phe	Cys	Phe	Gly	Met	Asp	Ile	Leu	Leu	Lys	Leu	Asp	Leu	Asp
		420					425					430			
Ala	Thr	Arg	Arg	Phe	Phe	Asp	Ala	Phe	Phe	Asp	Leu	Gln	Pro	His	Tyr
	435					440						445			
Trp	His	Gly	Phe	Leu	Ser	Ser	Arg	Leu	Phe	Leu	Pro	Glu	Leu	Leu	Val
	450					455					460				
Phe	Gly	Leu	Ser	Leu	Phe	Ser	His	Ala	Ser	Asn	Thr	Ser	Arg	Leu	Glu
465					470					475					480
Ile	Met	Thr	Lys	Gly	Thr	Val	Pro	Leu	Ala	Lys	Met	Ile	Asn	Asn	Leu
			485						490					495	
Val	Gln	Asp	Arg												
		500													

<210> 31
 <211> 1550
 <212> DNA
 <213> Citrus X paradisi

<220>
 <221> CDS
 <222> (45)..(1355)
 <223> coding for epsilon-cyclase

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 Met Asp Met Phe
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 ata cta ccg cca ata tca att ggt aat ggt att ttg gat ttg gtg gtg 104
 Ile Leu Pro Pro Ile Ser Ile Gly Asn Gly Ile Leu Asp Leu Val Val
 5 10 15 20
 att ggt tgt ggc cca gct ggt ctt gct ttg gct gca gaa tca gcg aag 152

Ile	Gly	Cys	Gly	Pro	Ala	Gly	Leu	Ala	Leu	Ala	Ala	Glu	Ser	Ala	Lys	
				25					30					35		
ttg	gga	tta	aat	gtt	gga	ctt	att	ggc	ccg	gat	ctc	cct	ttc	aca	aac	200
Leu	Gly	Leu	Asn	Val	Gly	Leu	Ile	Gly	Pro	Asp	Leu	Pro	Phe	Thr	Asn	
			40					45					50			
aat	tat	ggg	gtg	tgg	gaa	gat	gaa	ttt	aga	gat	ctt	gga	ctt	gaa	ggg	248
Asn	Tyr	Gly	Val	Trp	Glu	Asp	Glu	Phe	Arg	Asp	Leu	Gly	Leu	Glu	Gly	
		55					60					65				
tgt	atc	gaa	cat	gtc	tgg	aga	gac	aca	gtt	gta	tat	att	gat	gaa	gat	296
Cys	Ile	Glu	His	Val	Trp	Arg	Asp	Thr	Val	Val	Tyr	Ile	Asp	Glu	Asp	
	70					75					80					
gaa	ccc	atc	ttg	att	ggg	cgt	gct	tat	gga	cga	gtt	agt	cga	cat	ttg	344
Glu	Pro	Ile	Leu	Ile	Gly	Arg	Ala	Tyr	Gly	Arg	Val	Ser	Arg	His	Leu	
	85				90				95						100	
ctt	cat	gaa	gaa	tta	tta	aga	agg	tgt	gtc	gag	tca	ggg	gtt	tca	tat	392
Leu	His	Glu	Glu	Leu	Leu	Arg	Arg	Cys	Val	Glu	Ser	Gly	Val	Ser	Tyr	
				105				110					115			
ctt	agc	tca	aaa	gtg	gaa	agc	att	acg	gaa	tct	acc	agt	ggg	cat	cgt	440
Leu	Ser	Ser	Lys	Val	Glu	Ser	Ile	Thr	Glu	Ser	Thr	Ser	Gly	His	Arg	
			120					125					130			
ctt	gta	gct	tgt	gaa	cat	gat	atg	att	gtc	ccc	tgc	agg	ctt	gct	act	488
Leu	Val	Ala	Cys	Glu	His	Asp	Met	Ile	Val	Pro	Cys	Arg	Leu	Ala	Thr	
		135				140					145					
gtt	gct	tct	gga	gca	gca	tca	ggg	aag	cta	ttg	gaa	tat	gag	gtg	ggg	536
Val	Ala	Ser	Gly	Ala	Ala	Ser	Gly	Lys	Leu	Leu	Glu	Tyr	Glu	Val	Gly	
	150					155			160							
ggg	ccc	aaa	gtt	tct	gtc	caa	aca	gct	tat	ggg	gtg	gag	gtt	gag	gtg	584
Gly	Pro	Lys	Val	Ser	Val	Gln	Thr	Ala	Tyr	Gly	Val	Glu	Val	Glu	Val	
	165				170				175						180	
gaa	aat	aat	cca	tat	gat	cca	agc	ctt	atg	gtt	ttc	atg	gac	tac	aga	632
Glu	Asn	Asn	Pro	Tyr	Asp	Pro	Ser	Leu	Met	Val	Phe	Met	Asp	Tyr	Arg	
			185					190					195			
gac	tgt	act	aag	caa	gaa	gtt	cca	tct	ttt	gaa	tct	gac	aat	cca	aca	680
Asp	Cys	Thr	Lys	Gln	Glu	Val	Pro	Ser	Phe	Glu	Ser	Asp	Asn	Pro	Thr	
			200				205						210			
ttt	ctt	tat	gtc	atg	ccc	atg	tct	tca	aca	aga	gtt	ttc	ttt	gag	gaa	728
Phe	Leu	Tyr	Val	Met	Pro	Met	Ser	Ser	Thr	Arg	Val	Phe	Phe	Glu	Glu	
		215				220						225				
act	tgt	ttg	gca	tcg	aaa	gat	ggg	tta	cgt	ttt	gac	ata	ttg	aag	aaa	776
Thr	Cys	Leu	Ala	Ser	Lys	Asp	Gly	Leu	Arg	Phe	Asp	Ile	Leu	Lys	Lys	
	230				235						240					
aag	ctc	atg	gca	agg	tta	gag	aga	ttg	gga	atc	cag	gtt	ttg	aaa	act	824
Lys	Leu	Met	Ala	Arg	Leu	Glu	Arg	Leu	Gly	Ile	Gln	Val	Leu	Lys	Thr	
	245			250				255							260	
tat	gaa	gag	gaa	tgg	tca	tat	att	cca	gtt	ggg	ggg	tcc	tta	cca	aat	872
Tyr	Glu	Glu	Glu	Trp	Ser	Tyr	Ile	Pro	Val	Gly	Gly	Ser	Leu	Pro	Asn	
				265				270					275			
aca	gaa	caa	aga	aac	ctc	gca	ttt	ggg	gct	gct	gct	agc	atg	gtg	cat	920
Thr	Glu	Gln	Arg	Asn	Leu	Ala	Phe	Gly	Ala	Ala	Ala	Ser	Met	Val	His	
			280					285					290			
cca	gcc	act	ggc	tac	tca	gta	gtc	aga	tca	ctg	tca	gag	gct	cca	aac	968
Pro	Ala	Thr	Gly	Tyr	Ser	Val	Val	Arg	Ser	Leu	Ser	Glu	Ala	Pro	Asn	
		295				300						305				
tat	gct	tct	gca	att	gca	tat	ata	ttg	aaa	cac	gat	cat	tcc	aga	ggg	1016
Tyr	Ala	Ser	Ala	Ile	Ala	Tyr	Ile	Leu	Lys	His	Asp	His	Ser	Arg	Gly	
		310				315						320				
aga	ctt	aca	cat	gaa	caa	agt	aat	gag	aat	atc	tca	atg	caa	gct	tgg	1064
Arg	Leu	Thr	His	Glu	Gln	Ser	Asn	Glu	Asn	Ile	Ser	Met	Gln	Ala	Trp	
	325				330					335					340	
aat	act	ctc	tgg	cca	cag	gaa	agg	aag	cgc	caa	aga	gct	ttt	ttc	ctc	1112

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Asn Thr Leu Trp Pro Gln Glu Arg Lys Arg Gln Arg Ala Phe Phe Leu
      345                      350                      355
ttt gga cta gca ctc att ttg caa ctg gat att gag ggc atc agg aca 1160
Phe Gly Leu Ala Leu Ile Leu Gln Leu Asp Ile Glu Gly Ile Arg Thr
      360                      365                      370
ttc ttt cgc act ttc ttc cga tta ccc aag tgg atg tgg cac ggt ttc 1208
Phe Phe Arg Thr Phe Phe Arg Leu Pro Lys Trp Met Trp His Gly Phe
      375                      380                      385
ctt ggt tct agt ctc tca tca gcc gat ctc att cta ttt gcc ttc tat 1256
Leu Gly Ser Ser Leu Ser Ser Ala Asp Leu Ile Leu Phe Ala Phe Tyr
      390                      395                      400
atg ttt att ata gca cca aat gat ctg aga aag tgc ctt atc aga cat 1304
Met Phe Ile Ile Ala Pro Asn Asp Leu Arg Lys Cys Leu Ile Arg His
      405                      410                      415                      420
cta gtt tca gat cca act gga gca act atg gta aga aca tac ctg act 1352
Leu Val Ser Asp Pro Thr Gly Ala Thr Met Val Arg Thr Tyr Leu Thr
      425                      430                      435
tta tagttagttt gtattttcca tatttcagcc cttgtttggt atattttgga 1405
Leu
ttgccatacg tgacacataa tgagcttgta tatatactcc atgtatactg taaactgtta 1465
gtttgacaaa tgaagccctt ttttattttt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1525
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<210> 32
<211> 437
<212> PRT
<213> Citrus X paradisi

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<400> 32
Met Asp Met Phe Ile Leu Pro Pro Ile Ser Ile Gly Asn Gly Ile Leu
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Asp Leu Val Val Ile Gly Cys Gly Pro Ala Gly Leu Ala Leu Ala Ala
      20          25          30
Glu Ser Ala Lys Leu Gly Leu Asn Val Gly Leu Ile Gly Pro Asp Leu
      35          40          45
Pro Phe Thr Asn Asn Tyr Gly Val Trp Glu Asp Glu Phe Arg Asp Leu
      50          55          60
Gly Leu Glu Gly Cys Ile Glu His Val Trp Arg Asp Thr Val Val Tyr
      65          70          75          80
Ile Asp Glu Asp Glu Pro Ile Leu Ile Gly Arg Ala Tyr Gly Arg Val
      85          90          95
Ser Arg His Leu Leu His Glu Glu Leu Leu Arg Arg Cys Val Glu Ser
      100          105          110
Gly Val Ser Tyr Leu Ser Ser Lys Val Glu Ser Ile Thr Glu Ser Thr
      115          120          125
Ser Gly His Arg Leu Val Ala Cys Glu His Asp Met Ile Val Pro Cys
      130          135          140
Arg Leu Ala Thr Val Ala Ser Gly Ala Ala Ser Gly Lys Leu Leu Glu
      145          150          155          160
Tyr Glu Val Gly Gly Pro Lys Val Ser Val Gln Thr Ala Tyr Gly Val
      165          170          175
Glu Val Glu Val Glu Asn Asn Pro Tyr Asp Pro Ser Leu Met Val Phe
      180          185          190
Met Asp Tyr Arg Asp Cys Thr Lys Glu Glu Val Pro Ser Phe Glu Ser
      195          200          205
Asp Asn Pro Thr Phe Leu Tyr Val Met Pro Met Ser Ser Thr Arg Val
      210          215          220
Phe Phe Glu Glu Thr Cys Leu Ala Ser Lys Asp Gly Leu Arg Phe Asp

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225		230		235		240
Ile Leu Lys Lys Lys	Leu Met Ala Arg	Leu Glu Arg Leu Gly	Ile Gln			
	245	250	255			
Val Leu Lys Thr Tyr	Glu Glu Glu Trp	Ser Tyr Ile Pro	Val Gly Gly			
	260	265	270			
Ser Leu Pro Asn Thr	Glu Gln Arg Asn	Leu Ala Phe Gly	Ala Ala Ala			
	275	280	285			
Ser Met Val His Pro	Ala Thr Gly Tyr	Ser Val Val Arg	Ser Leu Ser			
	290	295	300			
Glu Ala Pro Asn Tyr	Ala Ser Ala Ile	Ala Tyr Ile Leu	Lys His Asp			
305	310	315	320			
His Ser Arg Gly Arg	Leu Thr His Glu	Gln Ser Asn Glu	Asn Ile Ser			
	325	330	335			
Met Gln Ala Trp Asn	Thr Leu Trp Pro	Gln Glu Arg Lys	Arg Gln Arg			
	340	345	350			
Ala Phe Phe Leu Phe	Gly Leu Ala Leu	Ile Leu Gln Leu	Asp Ile Glu			
	355	360	365			
Gly Ile Arg Thr Phe	Phe Arg Thr Phe	Phe Arg Leu Pro	Lys Trp Met			
	370	375	380			
Trp His Gly Phe Leu	Gly Ser Ser Leu	Ser Ser Ala Asp	Leu Ile Leu			
385	390	395	400			
Phe Ala Phe Tyr Met	Phe Ile Ile Ala	Pro Asn Asp Leu	Arg Lys Cys			
	405	410	415			
Leu Ile Arg His Leu	Val Ser Asp Pro	Thr Gly Ala Thr	Met Val Arg			
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Thr Tyr Leu Thr Leu						
	435					

<210> 33
 <211> 1830
 <212> DNA
 <213> Citrus X paradisi

<220>
 <221> CDS
 <222> (89)..(1660)
 <223> coding for epsilon-cyclase

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 tttccgtaag caacttctgg gctgaaaa atg ctc cca ttt ctc tcc tct ctg 112
 Met Leu Pro Phe Leu Ser Ser Leu
 1 5
 ctt aat gga gtc acg gat aac cct tgt agg aaa gcc atg gat act tta 160
 Leu Asn Gly Val Thr Asp Asn Pro Cys Arg Lys Ala Met Asp Thr Leu
 10 15 20
 ctc aaa act cat aac aag ctt gaa ttc ttg ccc caa gtt cac ggg gct 208
 Leu Lys Thr His Asn Lys Leu Glu Phe Leu Pro Gln Val His Gly Ala
 25 30 35 40
 ttg gaa aaa tcc agt agt tta agc tca ttg aag att cag aac cag gag 256
 Leu Glu Lys Ser Ser Ser Leu Ser Ser Leu Lys Ile Gln Asn Gln Glu
 45 50 55
 ctt agg ttt ggt ctc aag aag tct cgt caa aag agg aat agg agt tgt 304
 Leu Arg Phe Gly Leu Lys Lys Ser Arg Gln Lys Arg Asn Arg Ser Cys
 60 65 70
 ttc att aag gct agt agt agt gct ctt ttg gag cta gtt cct gaa acc 352
 Phe Ile Lys Ala Ser Ser Ser Ala Leu Leu Glu Leu Val Pro Glu Thr
 75 80 85

aag aag gaa aat ctt gaa ttt gag ctt ccc atg tat gac cca tca aag	400
Lys Lys Glu Asn Leu Glu Phe Glu Leu Pro Met Tyr Asp Pro Ser Lys	
90 95 100	
ggc ctt gtt gta gac cta gca gtt gtc ggt ggc ggc ccg gct ggg ctt	448
Gly Leu Val Val Asp Leu Ala Val Val Gly Gly Gly Pro Ala Gly Leu	
105 110 115 120	
gct gtt gct cag caa gtt tca ggg gcg ggg ctt tcg gtt tgc tcg att	496
Ala Val Ala Gln Gln Val Ser Gly Ala Gly Leu Ser Val Cys Ser Ile	
125 130 135	
gat cca tct ccc aaa ttg att tgg cca aat aat tat ggt gtt tgg gtg	544
Asp Pro Ser Pro Lys Leu Ile Trp Pro Asn Asn Tyr Gly Val Trp Val	
140 145 150	
gat gaa ttt gag gcc atg gat ttg ctt gat tgc ctt gat act act tgg	592
Asp Glu Phe Glu Ala Met Asp Leu Leu Asp Cys Leu Asp Thr Thr Trp	
155 160 165	
tct ggt gct gtt gtg cac att gat gat aat aca aag aag gat ctt aat	640
Ser Gly Ala Val Val His Ile Asp Asp Asn Thr Lys Lys Asp Leu Asn	
170 175 180	
aga cct tat ggg aga gtt aat agg aag ttg ctg aag tcg aaa atg ctg	688
Arg Pro Tyr Gly Arg Val Asn Arg Lys Leu Leu Lys Ser Lys Met Leu	
185 190 195 200	
caa aaa tgc ata acc aat ggt gtt aag ttt cac caa gct aaa gtt att	736
Gln Lys Cys Ile Thr Asn Gly Val Lys Phe His Gln Ala Lys Val Ile	
205 210 215	
aag gtt att cat gaa gag tcc aaa tct ttg ttg att tgc aat gat ggt	784
Lys Val Ile His Glu Glu Ser Lys Ser Leu Leu Ile Cys Asn Asp Gly	
220 225 230	
gtg aca att cag gca gcc gtg gtt ctt gat gct acg ggg ttc tct agg	832
Val Thr Ile Gln Ala Ala Val Val Leu Asp Ala Thr Gly Phe Ser Arg	
235 240 245	
tgt ctt gtc cag tat gat aag ccc tat aat cca ggt tac caa gtg gca	880
Cys Leu Val Gln Tyr Asp Lys Pro Tyr Asn Pro Gly Tyr Gln Val Ala	
250 255 260	
tat gga ata cta gct gag gta gaa cag cac ccg ttt gat tta gac aag	928
Tyr Gly Ile Leu Ala Glu Val Glu Gln His Pro Phe Asp Leu Asp Lys	
265 270 275 280	
atg gtt ttc atg gat tgg aga gat tcg cat ctg aac aac aat tcg cag	976
Met Val Phe Met Asp Trp Arg Asp Ser His Leu Asn Asn Asn Ser Gln	
285 290 295	
ctc aaa gag gca aat agc aaa att cct act ttt ctt tat gcc atg ccc	1024
Leu Lys Glu Ala Asn Ser Lys Ile Pro Thr Phe Leu Tyr Ala Met Pro	
300 305 310	
ttt tcg tca aac agg ata ttt ctt gaa gag act tcg cta gtg gcg cgg	1072
Phe Ser Ser Asn Arg Ile Phe Leu Glu Glu Thr Ser Leu Val Ala Arg	
315 320 325	
cct gga gtg cca atg aaa gat atc cag gaa aga atg gtg gct aga tta	1120
Pro Gly Val Pro Met Lys Asp Ile Gln Glu Arg Met Val Ala Arg Leu	
330 335 340	
aag cac tta ggc ata aaa gtt aaa agc att gaa gag gat gag cat tgt	1168
Lys His Leu Gly Ile Lys Val Lys Ser Ile Glu Glu Asp Glu His Cys	
345 350 355 360	
gtc att ccg atg ggt ggg ccc ctt cca gtg ctt cct caa aga gtt gtt	1216
Val Ile Pro Met Gly Gly Pro Leu Pro Val Leu Pro Gln Arg Val Val	
365 370 375	
gga ata ggt ggt acc gct ggg atg gtg cac cct tca act ggc tat atg	1264
Gly Ile Gly Gly Thr Ala Gly Met Val His Pro Ser Thr Gly Tyr Met	
380 385 390	
gtg gca agg act tta gct gcg gct cct att gtt gca aat gca atc gtt	1312
Val Ala Arg Thr Leu Ala Ala Ala Pro Ile Val Ala Asn Ala Ile Val	
395 400 405	

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cga agc ctc agt tct gac aga agc att tca gga cac aaa ttg tct gct 1360
Arg Ser Leu Ser Ser Asp Arg Ser Ile Ser Gly His Lys Leu Ser Ala
  410                      415                      420
gaa gtt tgg aaa gat ttg tgg ccc ata gaa agg aga agg caa agg gag 1408
Glu Val Trp Lys Asp Leu Trp Pro Ile Glu Arg Arg Arg Gln Arg Glu
  425                      430                      435                      440
ttc ttc tgt ttt ggt atg gat atc ctg ctc aaa ctt gac tta cct gcc 1456
Phe Phe Cys Phe Gly Met Asp Ile Leu Leu Lys Leu Asp Leu Pro Ala
                      445                      450                      455
act agg agg ttt ttc gat gct ttt ttt gat ctg gag cct cgt tat tgg 1504
Thr Arg Arg Phe Phe Asp Ala Phe Phe Asp Leu Glu Pro Arg Tyr Trp
                      460                      465                      470
cat ggt ttc tta tca tcg aga ttg ttt ctc ccc gag ctt tta gtt ttt 1552
His Gly Phe Leu Ser Ser Arg Leu Phe Leu Pro Glu Leu Leu Val Phe
                      475                      480                      485
ggg ctt tct cta ttc tca cat gcc tct aat act tct agg cta gag atc 1600
Gly Leu Ser Leu Phe Ser His Ala Ser Asn Thr Ser Arg Leu Glu Ile
  490                      495                      500
atg gca aag gga act ctt cct ttg gtt aac atg atc aac aac ttg gta 1648
Met Ala Lys Gly Thr Leu Pro Leu Val Asn Met Ile Asn Asn Leu Val
  505                      510                      515                      520
caa gat aca gat taagggtgacc atgatagtta taatgtgctt aataactcat 1700
Gln Asp Thr Asp
gcactaatcg tttataaaac acttcaaatt agttttgatg tttatagctt attacatgaa 1760
ccaaagctta tgatagacgt gctttggtat ttaagagttt cagccaaaaa aaaaaaaaaa 1820
aaaaaaaaaa 1830

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<210> 34

<211> 524

<212> PRT

<213> Citrus X paradisi

<400> 34

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Met Leu Pro Phe Leu Ser Ser Leu Leu Asn Gly Val Thr Asp Asn Pro
  1                      5                      10                      15
Cys Arg Lys Ala Met Asp Thr Leu Leu Lys Thr His Asn Lys Leu Glu
                      20                      25                      30
Phe Leu Pro Gln Val His Gly Ala Leu Glu Lys Ser Ser Ser Leu Ser
                      35                      40                      45
Ser Leu Lys Ile Gln Asn Gln Glu Leu Arg Phe Gly Leu Lys Lys Ser
                      50                      55                      60
Arg Gln Lys Arg Asn Arg Ser Cys Phe Ile Lys Ala Ser Ser Ser Ala
                      65                      70                      75                      80
Leu Leu Glu Leu Val Pro Glu Thr Lys Lys Glu Asn Leu Glu Phe Glu
                      85                      90                      95
Leu Pro Met Tyr Asp Pro Ser Lys Gly Leu Val Val Asp Leu Ala Val
                      100                      105                      110
Val Gly Gly Gly Pro Ala Gly Leu Ala Val Ala Gln Gln Val Ser Gly
                      115                      120                      125
Ala Gly Leu Ser Val Cys Ser Ile Asp Pro Ser Pro Lys Leu Ile Trp
                      130                      135                      140
Pro Asn Asn Tyr Gly Val Trp Val Asp Glu Phe Glu Ala Met Asp Leu
                      145                      150                      155                      160
Leu Asp Cys Leu Asp Thr Thr Trp Ser Gly Ala Val Val His Ile Asp
                      165                      170                      175
Asp Asn Thr Lys Lys Asp Leu Asn Arg Pro Tyr Gly Arg Val Asn Arg
                      180                      185                      190
Lys Leu Leu Lys Ser Lys Met Leu Gln Lys Cys Ile Thr Asn Gly Val

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	195					200					205					
Lys	Phe	His	Gln	Ala	Lys	Val	Ile	Lys	Val	Ile	His	Glu	Glu	Ser	Lys	
	210					215					220					
Ser	Leu	Leu	Ile	Cys	Asn	Asp	Gly	Val	Thr	Ile	Gln	Ala	Ala	Val	Val	
225					230					235					240	
Leu	Asp	Ala	Thr	Gly	Phe	Ser	Arg	Cys	Leu	Val	Gln	Tyr	Asp	Lys	Pro	
				245					250					255		
Tyr	Asn	Pro	Gly	Tyr	Gln	Val	Ala	Tyr	Gly	Ile	Leu	Ala	Glu	Val	Glu	
			260					265					270			
Gln	His	Pro	Phe	Asp	Leu	Asp	Lys	Met	Val	Phe	Met	Asp	Trp	Arg	Asp	
	275					280					285					
Ser	His	Leu	Asn	Asn	Asn	Ser	Gln	Leu	Lys	Glu	Ala	Asn	Ser	Lys	Ile	
	290					295					300					
Pro	Thr	Phe	Leu	Tyr	Ala	Met	Pro	Phe	Ser	Ser	Asn	Arg	Ile	Phe	Leu	
305					310					315					320	
Glu	Glu	Thr	Ser	Leu	Val	Ala	Arg	Pro	Gly	Val	Pro	Met	Lys	Asp	Ile	
				325					330					335		
Gln	Glu	Arg	Met	Val	Ala	Arg	Leu	Lys	His	Leu	Gly	Ile	Lys	Val	Lys	
			340					345					350			
Ser	Ile	Glu	Glu	Asp	Glu	His	Cys	Val	Ile	Pro	Met	Gly	Gly	Pro	Leu	
	355					360					365					
Pro	Val	Leu	Pro	Gln	Arg	Val	Val	Gly	Ile	Gly	Gly	Thr	Ala	Gly	Met	
	370					375					380					
Val	His	Pro	Ser	Thr	Gly	Tyr	Met	Val	Ala	Arg	Thr	Leu	Ala	Ala	Ala	
385					390					395					400	
Pro	Ile	Val	Ala	Asn	Ala	Ile	Val	Arg	Ser	Leu	Ser	Ser	Asp	Arg	Ser	
				405					410					415		
Ile	Ser	Gly	His	Lys	Leu	Ser	Ala	Glu	Val	Trp	Lys	Asp	Leu	Trp	Pro	
			420					425					430			
Ile	Glu	Arg	Arg	Arg	Gln	Arg	Glu	Phe	Phe	Cys	Phe	Gly	Met	Asp	Ile	
	435					440					445					
Leu	Leu	Lys	Leu	Asp	Leu	Pro	Ala	Thr	Arg	Arg	Phe	Phe	Asp	Ala	Phe	
	450					455					460					
Phe	Asp	Leu	Glu	Pro	Arg	Tyr	Trp	His	Gly	Phe	Leu	Ser	Ser	Arg	Leu	
465					470					475					480	
Phe	Leu	Pro	Glu	Leu	Leu	Val	Phe	Gly	Leu	Ser	Leu	Phe	Ser	His	Ala	
				485					490					495		
Ser	Asn	Thr	Ser	Arg	Leu	Glu	Ile	Met	Ala	Lys	Gly	Thr	Leu	Pro	Leu	
	500					505					510					
Val	Asn	Met	Ile	Asn	Asn	Leu	Val	Gln	Asp	Thr	Asp					
	515					520										

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<210> 35
<211> 787
<212> DNA
<213> Citrus sinensis
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<220>
<221> CDS
<222> (2)..(787)
<223> coding for epsilon-cyclase (partial)
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<400> 35
t ctt gct ttg gct gca gaa tca gcg aag ttg gga tta aat gtt gga ctt 49
Leu Ala Leu Ala Ala Glu Ser Ala Lys Leu Gly Leu Asn Val Gly Leu
1 5 10 15
att ggc ccg gat ctc cct ttc aca aac aat tat ggt gtg tgg gaa gat 97
Ile Gly Pro Asp Leu Pro Phe Thr Asn Asn Tyr Gly Val Trp Glu Asp

	20		25		30	
gaa ttt aga gat ctt gga ctt gaa ggg tgt atc gaa caa gtc tgg aga						145
Glu Phe Arg Asp Leu Gly Leu Glu Gly Cys Ile Glu Gln Val Trp Arg						
	35		40		45	
gac aca gtt gta tat att gat gaa gat gaa ccc atc ttg att ggt cgt						193
Asp Thr Val Val Tyr Ile Asp Glu Asp Glu Pro Ile Leu Ile Gly Arg						
	50		55		60	
gct tat gga cga gtt agt cga cat ttg ctt cat gaa gaa tta tta aga						241
Ala Tyr Gly Arg Val Ser Arg His Leu Leu His Glu Glu Leu Leu Arg						
	65		70		75	80
agg tgt gtc gag tca ggt gta tca tat ctt agc tca aaa gtg gaa agc						289
Arg Cys Val Glu Ser Gly Val Ser Tyr Leu Ser Ser Lys Val Glu Ser						
	85		90		95	
att acg gaa tct acc agt ggt cat cgt ctt gta gct tgt gaa cat gat						337
Ile Thr Glu Ser Thr Ser Gly His Arg Leu Val Ala Cys Glu His Asp						
	100		105		110	
atg att gtc ccc tgc agg ctt gct act gtt gct tct gga gca gca tca						385
Met Ile Val Pro Cys Arg Leu Ala Thr Val Ala Ser Gly Ala Ala Ser						
	115		120		125	
ggg aag cta ttg gaa tat ggg gtg ggg ggt ccc aaa gtt tct gtc caa						433
Gly Lys Leu Leu Glu Tyr Gly Val Gly Gly Pro Lys Val Ser Val Gln						
	130		135		140	
aca gct tat ggt gtg gag gtt gag gtg gaa aat aat cca tat gat cca						481
Thr Ala Tyr Gly Val Glu Val Glu Val Glu Asn Asn Pro Tyr Asp Pro						
	145		150		155	160
agc ctt atg gtt ttc atg gac tac aga gac tgt act aag caa gaa gtt						529
Ser Leu Met Val Phe Met Asp Tyr Arg Asp Cys Thr Lys Gln Glu Val						
	165		170		175	
cca tct ttt gaa tct gac aat cca aca ttt ctt tat gtc atg ccc atg						577
Pro Ser Phe Glu Ser Asp Asn Pro Thr Phe Leu Tyr Val Met Pro Met						
	180		185		190	
tct tca aca aga gtt ttc ttt gag gaa act tgt ttg gca tcg aaa gat						625
Ser Ser Thr Arg Val Phe Phe Glu Glu Thr Cys Leu Ala Ser Lys Asp						
	195		200		205	
ggc tta cgt ttt gac ata ttg aag aaa aag ctc atg gca agg tta gag						673
Gly Leu Arg Phe Asp Ile Leu Lys Lys Lys Leu Met Ala Arg Leu Glu						
	210		215		220	
aga ttg gga atc cag gtt ttg aaa act tat gaa gag gaa tgg tca tat						721
Arg Leu Gly Ile Gln Val Leu Lys Thr Tyr Glu Glu Glu Trp Ser Tyr						
	225		230		235	240
att cca gtt ggt ggt tcc tta cca aat aca gaa caa aga aac ctc gca						769
Ile Pro Val Gly Gly Ser Leu Pro Asn Thr Glu Gln Arg Asn Leu Ala						
	245		250		255	
tat ggt gct gct gct agc						787
Tyr Gly Ala Ala Ala Ser						
	260					

<210> 36

<211> 262

<212> PRT

<213> Citrus sinensis

<400> 36

Leu Ala Leu Ala Ala Glu Ser Ala Lys Leu Gly Leu Asn Val Gly Leu	
1 5 10 15	
Ile Gly Pro Asp Leu Pro Phe Thr Asn Asn Tyr Gly Val Trp Glu Asp	
20 25 30	
Glu Phe Arg Asp Leu Gly Leu Glu Gly Cys Ile Glu Gln Val Trp Arg	

[illegible]

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<210> 37
<211> 2357
<212> DNA
<213> Spinacia oleracea
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<220>
<221> CDS
<222> (264)..(1814)
<223> coding for epsilon-cyclase
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<400> 37																		
gcacgagaca	ccacaaaacc	attgaggaga	gagaaagtca	accaaatttc	acaccttcca													60
cctccctctt	ccatggccgc	aacccaaacc	cagccacctt	caccgccgcc	gtcgacagca													120
caactgaactt	caccactaca	aacttaaaaa	aaatcttgga	gaaatttgat	tccgtaaaaa													180
tggagtatta	ttgtctcgga	gcttcgaaat	tcgcaacaat	ggcggtttct	cctgcgctta													240
atcacgacaa	tttgaggaat	aaa atg gtt	aaa caa cgc	cag aat ttc	cag acg													293
Met Val Lys Gln Arg Gln Asn Phe Gln Thr																		
ttt tgc ttt	tgg agg ccg	aat tct tgc	aac gtt gta	gta gaa tgt	agt													341
Phe Cys Phe	Trp Arg Pro	Asn Ser Ser	Asn Val Val	Val Val Glu	Cys Ser													
agt cgt agg	agt gga agt	agt gtt ttg	agg agt gcg	aat agc gac	agt													389
Ser Arg Arg	Ser Gly Ser	Ser Val Leu	Arg Ser Ala	Asn Ser Asp	Ser													
agt tgc gta	att gcg cca	gag gat ttt	gcg aac gaa	gaa gat ttc	atc													437
Ser Cys Val	Ile Ala Pro	Glu Asp Phe	Ala Asn Glu	Glu Asp Phe	Ile													
aaa gct ggt	ggt tcc gag	ctt ctt tat	gtt caa atg	caq caq aat	aaa													485

Lys	Ala	Gly	Gly	Ser	Glu	Leu	Leu	Tyr	Val	Gln	Met	Gln	Gln	Asn	Lys	
60						65					70					
gct	atg	gat	tgt	tac	tcc	aaa	att	tcc	gat	aag	ctg	cgt	caa	ata	tca	533
Ala	Met	Asp	Cys	Tyr	Ser	Lys	Ile	Ser	Asp	Lys	Leu	Arg	Gln	Ile	Ser	
75						80					85				90	
gat	gcc	aat	gaa	ctg	ctg	gat	atg	gtg	gtt	att	ggg	tgt	ggg	cca	gct	581
Asp	Ala	Asn	Glu	Leu	Leu	Asp	Met	Val	Val	Ile	Gly	Cys	Gly	Pro	Ala	
				95					100					105		
ggg	cta	gct	ttg	gct	gca	gaa	tcg	gct	aaa	ctt	gga	tta	aaa	ggt	ggc	629
Gly	Leu	Ala	Leu	Ala	Ala	Glu	Ser	Ala	Lys	Leu	Gly	Leu	Lys	Val	Gly	
			110					115					120			
ctt	ggt	ggg	cct	gat	ctt	cct	ttt	acg	aat	aac	tac	ggc	ggt	tgg	gaa	677
Leu	Val	Gly	Pro	Asp	Leu	Pro	Phe	Thr	Asn	Asn	Tyr	Gly	Val	Trp	Glu	
		125					130				135					
gat	gaa	ttc	aga	gca	ttg	gga	ctt	gga	ggc	tgt	atc	gag	cac	ggt	tgg	725
Asp	Glu	Phe	Arg	Ala	Leu	Gly	Leu	Gly	Gly	Cys	Ile	Glu	His	Val	Trp	
	140					145				150						
cgt	gat	acc	att	gtg	tat	att	gat	gat	gac	aat	cct	ata	tat	att	ggg	773
Arg	Asp	Thr	Ile	Val	Tyr	Ile	Asp	Asp	Asp	Asn	Pro	Ile	Tyr	Ile	Gly	
155					160					165					170	
cga	tct	tat	gga	aaa	gtc	agc	cgg	caa	tta	ctt	cac	aag	gaa	ctg	gtg	821
Arg	Ser	Tyr	Gly	Lys	Val	Ser	Arg	Gln	Leu	Leu	His	Lys	Glu	Leu	Val	
				175				180						185		
cac	agg	tgt	ttg	gag	tca	ggg	gtc	tct	tat	ctg	aat	gcg	aaa	gtg	gaa	869
His	Arg	Cys	Leu	Glu	Ser	Gly	Val	Ser	Tyr	Leu	Asn	Ala	Lys	Val	Glu	
			190				195					200				
aat	att	atg	gaa	gga	cct	gat	gga	cat	agg	ctt	ggt	gct	tgt	gaa	cgt	917
Asn	Ile	Met	Glu	Gly	Pro	Asp	Gly	His	Arg	Leu	Val	Ala	Cys	Glu	Arg	
	205						210					215				
ggg	gtc	act	att	ccc	tgc	agg	ctt	gta	act	ggt	gca	tct	gga	gca	gct	965
Gly	Val	Thr	Ile	Pro	Cys	Arg	Leu	Val	Thr	Val	Ala	Ser	Gly	Ala	Ala	
	220					225					230					
tca	ggg	aaa	ctt	ctg	gag	tat	gaa	gtg	ggg	ggg	cca	agg	ggt	tgt	gta	1013
Ser	Gly	Lys	Leu	Leu	Glu	Tyr	Glu	Val	Gly	Gly	Pro	Arg	Val	Cys	Val	
235					240					245				250		
caa	aca	gct	tat	ggg	gtg	gag	gtg	gag	gtg	gaa	aac	agt	cct	tat	gat	1061
Gln	Thr	Ala	Tyr	Gly	Val	Glu	Val	Glu	Val	Glu	Asn	Ser	Pro	Tyr	Asp	
				255					260					265		
ccc	aat	gtg	atg	gtg	ttc	atg	gac	tac	aga	gac	tac	act	aaa	ctg	agc	1109
Pro	Asn	Val	Met	Val	Phe	Met	Asp	Tyr	Arg	Asp	Tyr	Thr	Lys	Leu	Ser	
			270					275					280			
ggt	caa	tct	ctg	gag	gca	aag	tat	cca	aca	ttc	ttg	tat	gca	atg	ccg	1157
Val	Gln	Ser	Leu	Glu	Ala	Lys	Tyr	Pro	Thr	Phe	Leu	Tyr	Ala	Met	Pro	
		285					290					295				
ata	tca	cca	act	agg	atc	ttc	ttt	gag	gag	act	tgc	ttg	gct	tca	gta	1205
Ile	Ser	Pro	Thr	Arg	Ile	Phe	Phe	Glu	Glu	Thr	Cys	Leu	Ala	Ser	Val	
		300				305					310					
gat	gca	atg	ccc	ttt	gac	ctg	ctc	aag	aaa	aag	ctt	atg	aca	aga	tta	1253
Asp	Ala	Met	Pro	Phe	Asp	Leu	Leu	Lys	Lys	Lys	Leu	Met	Thr	Arg	Leu	
	315				320					325					330	
caa	act	atg	ggg	ggt	cgt	atc	acc	aaa	ata	tat	gaa	gag	gag	tgg	tct	1301
Gln	Thr	Met	Gly	Val	Arg	Ile	Thr	Lys	Ile	Tyr	Glu	Glu	Glu	Trp	Ser	
			335					340						345		
tat	ata	cct	ggt	ggg	tcc	tta	cca	aat	aca	gag	caa	aga	aac	ctt		1349
Tyr	Ile	Pro	Val	Gly	Gly	Ser	Leu	Pro	Asn	Thr	Glu	Gln	Arg	Asn	Leu	
			350					355					360			
gca	ttt	ggg	gct	gct	gcg	agc	atg	gtg	cat	cca	gcc	aca	ggg	tat	tca	1397
Ala	Phe	Gly	Ala	Ala	Ala	Ser	Met	Val	His	Pro	Ala	Thr	Gly	Tyr	Ser	
		365					370					375				
gtc	gtg	aga	tca	ctg	tca	gaa	gct	cca	aag	tat	gct	tct	gca	att	gca	1445

Val	Val	Arg	Ser	Leu	Ser	Glu	Ala	Pro	Lys	Tyr	Ala	Ser	Ala	Ile	Ala		
380						385					390						
aac	ttg	atc	aag	aat	gac	ctg	tca	aaa	aat	gca	ata	ttg	cgt	cag	agg	1493	
Asn	Leu	Ile	Lys	Asn	Asp	Leu	Ser	Lys	Asn	Ala	Ile	Leu	Arg	Gln	Arg		
395				400					405					410			
agt	gtg	ggg	aat	atc	tca	atg	caa	gcc	tgg	aat	act	ctt	tgg	cca	caa	1541	
Ser	Val	Gly	Asn	Ile	Ser	Met	Gln	Ala	Trp	Asn	Thr	Leu	Trp	Pro	Gln		
			415						420					425			
gaa	agg	aaa	cgt	cag	aga	gca	ttc	ttc	ctg	ttc	gga	cta	tca	ctt	ata	1589	
Glu	Arg	Lys	Arg	Gln	Arg	Ala	Phe	Phe	Leu	Phe	Gly	Leu	Ser	Leu	Ile		
			430						435					440			
gtc	cag	ctt	gat	att	gag	ggg	atc	agg	aca	ttc	ttc	cgc	acc	ttc	ttc	1637	
Val	Gln	Leu	Asp	Ile	Glu	Gly	Ile	Arg	Thr	Phe	Phe	Arg	Thr	Phe	Phe		
	445						450					455					
cga	gtg	cca	aaa	tgg	atg	tgg	gag	gga	ttc	ctc	ggg	tct	aat	ctc	tct	1685	
Arg	Val	Pro	Lys	Trp	Met	Trp	Glu	Gly	Phe	Leu	Gly	Ser	Asn	Leu	Ser		
	460					465					470						
tca	gct	gat	ctc	ata	ttg	ttt	gcc	ttt	tat	atg	ttc	ttt	att	gct	ccg	1733	
Ser	Ala	Asp	Leu	Ile	Leu	Phe	Ala	Phe	Tyr	Met	Phe	Phe	Ile	Ala	Pro		
	475			480					485					490			
aat	gac	ttg	aga	atg	ggg	ctt	ata	agg	cat	cta	cta	tct	gat	cct	aca	1781	
Asn	Asp	Leu	Arg	Met	Gly	Leu	Ile	Arg	His	Leu	Leu	Ser	Asp	Pro	Thr		
			495					500					505				
ggg	gcg	acc	atg	ata	aga	acg	tac	ata	aca	cta	taaaagtaat	atgaaatgct	1834				
Gly	Ala	Thr	Met	Ile	Arg	Thr	Tyr	Ile	Thr	Leu							
	510					515											
cactcctttg	tacatcatgc	aaaatttggt	cgaattgact	ggactatgca	gtctaacttg	1894											
gtgtaaaaaa	aacacaatta	ataaattttt	tgtaggtgca	gcctctatac	ttgatattct	1954											
cgattcagat	ataatattgt	cagtattcct	cgttaaagat	cagttgtttc	tacaattcca	2014											
gaggtcctg	gaattggtgt	tacccttcca	tgtagctcat	tgataaatgt	tgagggtaga	2074											
ggctttttct	tagatgcttg	cttgacagctt	gctcatggat	atattcagtt	gttcagtaga	2134											
cacgttaaca	actactacag	tgggggcac	attgatctgg	accgggagag	ctgagcatct	2194											
atcacagggt	agccagctca	actacgtagg	tcaaccttga	gccactccca	aacatttttg	2254											
cagctgatgg	ggttcaccct	gtaagggtgag	tttcttacca	actccaccaa	cttatgttgg	2314											
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<210> 38

<211> 517

<212> PRT

<213> Spinacia oleracea

<400> 38

Met	Val	Lys	Gln	Arg	Gln	Asn	Phe	Gln	Thr	Phe	Cys	Phe	Trp	Arg	Pro		
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Asn	Ser	Ser	Asn	Val	Val	Val	Glu	Cys	Ser	Ser	Arg	Arg	Ser	Gly	Ser		
		20					25						30				
Ser	Val	Leu	Arg	Ser	Ala	Asn	Ser	Asp	Ser	Ser	Cys	Val	Ile	Ala	Pro		
	35					40					45						
Glu	Asp	Phe	Ala	Asn	Glu	Glu	Asp	Phe	Ile	Lys	Ala	Gly	Gly	Ser	Glu		
	50				55						60						
Leu	Leu	Tyr	Val	Gln	Met	Gln	Gln	Asn	Lys	Ala	Met	Asp	Cys	Tyr	Ser		
	65			70					75					80			
Lys	Ile	Ser	Asp	Lys	Leu	Arg	Gln	Ile	Ser	Asp	Ala	Asn	Glu	Leu	Leu		
			85					90					95				
Asp	Met	Val	Val	Ile	Gly	Cys	Gly	Pro	Ala	Gly	Leu	Ala	Leu	Ala	Ala		
	100						105						110				
Glu	Ser	Ala	Lys	Leu	Gly	Leu	Lys	Val	Gly	Leu	Val	Gly	Pro	Asp	Leu		
	115					120						125					

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Pro Phe Thr Asn Asn Tyr Gly Val Trp Glu Asp Glu Phe Arg Ala Leu
 130                      135                      140
Gly Leu Gly Gly Cys Ile Glu His Val Trp Arg Asp Thr Ile Val Tyr
145                      150                      155                      160
Ile Asp Asp Asp Asn Pro Ile Tyr Ile Gly Arg Ser Tyr Gly Lys Val
                      165                      170                      175
Ser Arg Gln Leu Leu His Lys Glu Leu Val His Arg Cys Leu Glu Ser
                      180                      185                      190
Gly Val Ser Tyr Leu Asn Ala Lys Val Glu Asn Ile Met Glu Gly Pro
                      195                      200                      205
Asp Gly His Arg Leu Val Ala Cys Glu Arg Gly Val Thr Ile Pro Cys
 210                      215                      220
Arg Leu Val Thr Val Ala Ser Gly Ala Ala Ser Gly Lys Leu Leu Glu
225                      230                      235                      240
Tyr Glu Val Gly Gly Pro Arg Val Cys Val Gln Thr Ala Tyr Gly Val
                      245                      250                      255
Glu Val Glu Val Glu Asn Ser Pro Tyr Asp Pro Asn Val Met Val Phe
 260                      265                      270
Met Asp Tyr Arg Asp Tyr Thr Lys Leu Ser Val Gln Ser Leu Glu Ala
 275                      280                      285
Lys Tyr Pro Thr Phe Leu Tyr Ala Met Pro Ile Ser Pro Thr Arg Ile
 290                      295                      300
Phe Phe Glu Glu Thr Cys Leu Ala Ser Val Asp Ala Met Pro Phe Asp
305                      310                      315                      320
Leu Leu Lys Lys Lys Leu Met Thr Arg Leu Gln Thr Met Gly Val Arg
                      325                      330                      335
Ile Thr Lys Ile Tyr Glu Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly
 340                      345                      350
Ser Leu Pro Asn Thr Glu Gln Arg Asn Leu Ala Phe Gly Ala Ala Ala
 355                      360                      365
Ser Met Val His Pro Ala Thr Gly Tyr Ser Val Val Arg Ser Leu Ser
 370                      375                      380
Glu Ala Pro Lys Tyr Ala Ser Ala Ile Ala Asn Leu Ile Lys Asn Asp
385                      390                      395                      400
Leu Ser Lys Asn Ala Ile Leu Arg Gln Arg Ser Val Gly Asn Ile Ser
                      405                      410                      415
Met Gln Ala Trp Asn Thr Leu Trp Pro Gln Glu Arg Lys Arg Gln Arg
 420                      425                      430
Ala Phe Phe Leu Phe Gly Leu Ser Leu Ile Val Gln Leu Asp Ile Glu
 435                      440                      445
Gly Ile Arg Thr Phe Phe Arg Thr Phe Phe Arg Val Pro Lys Trp Met
 450                      455                      460
Trp Glu Gly Phe Leu Gly Ser Asn Leu Ser Ser Ala Asp Leu Ile Leu
465                      470                      475                      480
Phe Ala Phe Tyr Met Phe Phe Ile Ala Pro Asn Asp Leu Arg Met Gly
                      485                      490                      495
Leu Ile Arg His Leu Leu Ser Asp Pro Thr Gly Ala Thr Met Ile Arg
 500                      505                      510
Thr Tyr Ile Thr Leu
 515

```

<210> 39

<211> 1378

<212> DNA

<213> Solanum tuberosum

<220>

<221> CDS

<222> (2)..(1147)

<223> coding for epsilon-cyclase (partial)

<400> 39

```

t agc ggn nnn nag gat gag ttc aaa gat ctt ggt ctt caa gcc tgc att 49
  Ser Xaa Xaa Xaa Asp Glu Phe Lys Asp Leu Gly Leu Gln Ala Cys Ile
    1           5           10          15
gaa cat gtt tgg cgg gat acc att gta tat ctt gat gat gat gat cct 97
Glu His Val Trp Arg Asp Thr Ile Val Tyr Leu Asp Asp Asp Asp Pro
    20          25          30
att ctt att ggc cgt gcc tat gga aga gtt agt cgc cat tta ctg cac 145
Ile Leu Ile Gly Arg Ala Tyr Gly Arg Val Ser Arg His Leu Leu His
    35          40          45
gag gag tta ctc aaa agg tgt gtg gag gca ggt gtt ttg tat cta aac 193
Glu Glu Leu Leu Lys Arg Cys Val Glu Ala Gly Val Leu Tyr Leu Asn
    50          55          60
tcg aaa gtg gat agg att gtt gag gcc aca aat ggc cac agt ctt gta 241
Ser Lys Val Asp Arg Ile Val Glu Ala Thr Asn Gly His Ser Leu Val
    65          70          75          80
gag tgc gag ggt gat gtt gtg att ccc tgc agg ttt gtg act gtt gca 289
Glu Cys Glu Gly Asp Val Val Ile Pro Cys Arg Phe Val Thr Val Ala
    85          90          95
tcg gga gca gcc tcg ggg aaa ttc ttg cag tat gag ttg gga ggt cct 337
Ser Gly Ala Ala Ser Gly Lys Phe Leu Gln Tyr Glu Leu Gly Gly Pro
    100         105         110
aga gtt tct gtt caa aca gct tat gga gtg gaa gtt gag gtc gat aac 385
Arg Val Ser Val Gln Thr Ala Tyr Gly Val Glu Val Glu Val Asp Asn
    115         120         125
aat cca ttt gac ccg agc ctg atg gtt ttc atg gat tat aga gac tat 433
Asn Pro Phe Asp Pro Ser Leu Met Val Phe Met Asp Tyr Arg Asp Tyr
    130         135         140
gtc aga cac gac gct caa tct tta gaa gct aaa tat cca aca ttt ctc 481
Val Arg His Asp Ala Gln Ser Leu Glu Ala Lys Tyr Pro Thr Phe Leu
    145         150         155         160
tat gcc atg ccc atg tct cca aca cga gtc ttt ttc gag gaa act tgt 529
Tyr Ala Met Pro Met Ser Pro Thr Arg Val Phe Phe Glu Glu Thr Cys
    165         170         175
ttg gct tca aaa gat gca atg cca ttc gat ctg tta aag aaa aaa ttg 577
Leu Ala Ser Lys Asp Ala Met Pro Phe Asp Leu Leu Lys Lys Lys Leu
    180         185         190
atg tta cga ttg aac acc ctc ggt gta aga att aaa gaa att tat gag 625
Met Leu Arg Leu Asn Thr Leu Gly Val Arg Ile Lys Glu Ile Tyr Glu
    195         200         205
gag gaa tgg tct tac ata cca gtt gga gga tct ttg cca aat aca gaa 673
Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser Leu Pro Asn Thr Glu
    210         215         220
caa aaa aca ctt gca ttt ggt gct gct gct agc atg gtt cat cca gcc 721
Gln Lys Thr Leu Ala Phe Gly Ala Ala Ala Ser Met Val His Pro Ala
    225         230         235         240
aca ggt tat tca gtc gtc aga tca ctg tct gaa gct cca aaa tgc gcc 769
Thr Gly Tyr Ser Val Val Arg Ser Leu Ser Glu Ala Pro Lys Cys Ala
    245         250         255
ttc gtg ctt gca aat ata tta cga caa aat cat agc aag aat atg ctt 817
Phe Val Leu Ala Asn Ile Leu Arg Gln Asn His Ser Lys Asn Met Leu
    260         265         270
act agt tca agt acc ccg agt att tca act caa gct tgg aac act ctt 865
Thr Ser Ser Ser Thr Pro Ser Ile Ser Thr Gln Ala Trp Asn Thr Leu
    275         280         285
tgg cca caa gaa cga aaa cga caa aga tcg ttt ttc cta ttt gga ctg 913
Trp Pro Gln Glu Arg Lys Arg Gln Arg Ser Phe Phe Leu Phe Gly Leu

```

```

      290              295              300
gct ctg ata ttg cag ctg gat att gag ggg ata agg tca ttt ttc cgc   961
Ala Leu Ile Leu Gln Leu Asp Ile Glu Gly Ile Arg Ser Phe Phe Arg
305              310              315              320
gcg ttc ttc cgt gtg cca aaa tgg atg tgg cag gga ttt ctt ggt tca   1009
Ala Phe Phe Arg Val Pro Lys Trp Met Trp Gln Gly Phe Leu Gly Ser
              325              330              335
agt ctt tct tna gca gac ctc atg tta ttt gcc ttc tac atg ttt att   1057
Ser Leu Ser Xaa Ala Asp Leu Met Leu Phe Ala Phe Tyr Met Phe Ile
              340              345              350
att gca cca aat gac atg aga aga ggc tta atc aga cat ctt tta tct   1105
Ile Ala Pro Asn Asp Met Arg Arg Gly Leu Ile Arg His Leu Leu Ser
              355              360              365
gat cct act ggt gca aca ttg ata aga act tat ctt aca ttt           1147
Asp Pro Thr Gly Ala Thr Leu Ile Arg Thr Tyr Leu Thr Phe
              370              375              380
tagagtaaatt tcctcctaca atagttgttg aannagaggc ctcattactt cagattcata 1207
acagaaatcg cggctctctcg aggccttgta tataacattt tcactagggtt aatattgctt 1267
gaataagttg cacagtttca gtttttgtat ctgcttcctt tttgtccaag atcatgtatt 1327
ganccaattt atatacattg ccagtatata taaattttat aaaaaaaaaa a           1378

```

<210> 40
 <211> 382
 <212> PRT
 <213> Solanum tuberosum

<220>
 <221> MISC_FEATURE
 <222> (2)..(4), (340)
 <223> each occurrence of Xaa is any amino acid

```

<400> 40
Ser Xaa Xaa Xaa Asp Glu Phe Lys Asp Leu Gly Leu Gln Ala Cys Ile
  1              5              10              15
Glu His Val Trp Arg Asp Thr Ile Val Tyr Leu Asp Asp Asp Asp Pro
              20              25              30
Ile Leu Ile Gly Arg Ala Tyr Gly Arg Val Ser Arg His Leu Leu His
              35              40              45
Glu Glu Leu Leu Lys Arg Cys Val Glu Ala Gly Val Leu Tyr Leu Asn
              50              55              60
Ser Lys Val Asp Arg Ile Val Glu Ala Thr Asn Gly His Ser Leu Val
              65              70              75              80
Glu Cys Glu Gly Asp Val Val Ile Pro Cys Arg Phe Val Thr Val Ala
              85              90              95
Ser Gly Ala Ala Ser Gly Lys Phe Leu Gln Tyr Glu Leu Gly Gly Pro
              100              105              110
Arg Val Ser Val Gln Thr Ala Tyr Gly Val Glu Val Glu Val Asp Asn
              115              120              125
Asn Pro Phe Asp Pro Ser Leu Met Val Phe Met Asp Tyr Arg Asp Tyr
              130              135              140
Val Arg His Asp Ala Gln Ser Leu Glu Ala Lys Tyr Pro Thr Phe Leu
              145              150              155              160
Tyr Ala Met Pro Met Ser Pro Thr Arg Val Phe Phe Glu Glu Thr Cys
              165              170              175
Leu Ala Ser Lys Asp Ala Met Pro Phe Asp Leu Leu Lys Lys Lys Leu
              180              185              190
Met Leu Arg Leu Asn Thr Leu Gly Val Arg Ile Lys Glu Ile Tyr Glu
              195              200              205

```

Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser Leu Pro Asn Thr Glu
 210 215 220
 Gln Lys Thr Leu Ala Phe Gly Ala Ala Ala Ser Met Val His Pro Ala
 225 230 235 240
 Thr Gly Tyr Ser Val Val Arg Ser Leu Ser Glu Ala Pro Lys Cys Ala
 245 250 255
 Phe Val Leu Ala Asn Ile Leu Arg Gln Asn His Ser Lys Asn Met Leu
 260 265 270
 Thr Ser Ser Ser Thr Pro Ser Ile Ser Thr Gln Ala Trp Asn Thr Leu
 275 280 285
 Trp Pro Gln Glu Arg Lys Arg Gln Arg Ser Phe Phe Leu Phe Gly Leu
 290 295 300
 Ala Leu Ile Leu Gln Leu Asp Ile Glu Gly Ile Arg Ser Phe Phe Arg
 305 310 315 320
 Ala Phe Phe Arg Val Pro Lys Trp Met Trp Gln Gly Phe Leu Gly Ser
 325 330 335
 Ser Leu Ser Xaa Ala Asp Leu Met Leu Phe Ala Phe Tyr Met Phe Ile
 340 345 350
 Ile Ala Pro Asn Asp Met Arg Arg Gly Leu Ile Arg His Leu Leu Ser
 355 360 365
 Asp Pro Thr Gly Ala Thr Leu Ile Arg Thr Tyr Leu Thr Phe
 370 375 380

<210> 41
 <211> 497
 <212> DNA
 <213> *Daucus carota*

<220>
 <221> CDS
 <222> (1)..(495)
 <223> coding for episilon-cyclase (partial)

<400> 41
 tat ggt gtt tgg gtg gat gaa ttt ata gat ctt gga ctt gaa ggg tgt 48
 Tyr Gly Val Trp Val Asp Glu Phe Ile Asp Leu Gly Leu Glu Gly Cys
 1 5 10 15
 att gag cat gtt tgg cgg gat act att gta tat ctt gat gat ggt gat 96
 Ile Glu His Val Trp Arg Asp Thr Ile Val Tyr Leu Asp Asp Gly Asp
 20 25 30
 cct att atg att ggc cgt gct tac gga aga gtt agt cgc cat ttg ctt 144
 Pro Ile Met Ile Gly Arg Ala Tyr Gly Arg Val Ser Arg His Leu Leu
 35 40 45
 cat gaa gaa ttg ctt aaa agg tgt gtc gag tca ggt gtt tcg tat ctt 192
 His Glu Glu Leu Leu Lys Arg Cys Val Glu Ser Gly Val Ser Tyr Leu
 50 55 60
 agc tca aaa gtt gaa aag att att gaa gct gga gat ggc cac agc ctg 240
 Ser Ser Lys Val Glu Lys Ile Ile Glu Ala Gly Asp Gly His Ser Leu
 65 70 75 80
 gtt gag tgt gaa aat aat att gtc att cca tgc agg ctt gct act gtt 288
 Val Glu Cys Glu Asn Asn Ile Val Ile Pro Cys Arg Leu Ala Thr Val
 85 90 95
 gca tct gga gca gct tct ggg aaa ctt ttg cag tat gag gtt ggg ggt 336
 Ala Ser Gly Ala Ala Ser Gly Lys Leu Leu Gln Tyr Glu Val Gly Gly
 100 105 110
 ccc aga gtt tct gtc caa aca gct tat ggt gtc gag gtt gag gtg gaa 384
 Pro Arg Val Ser Val Gln Thr Ala Tyr Gly Val Glu Val Glu Val Glu
 115 120 125

```

aac aat cca tat gat ccc agt cta atg gtt ttc atg gat tac aga gat 432
Asn Asn Pro Tyr Asp Pro Ser Leu Met Val Phe Met Asp Tyr Arg Asp
    130                135                140
tat acc aaa caa aaa gtt cca ggc atg gag gca gaa tat cca act ttc 480
Tyr Thr Lys Gln Lys Val Pro Gly Met Glu Ala Glu Tyr Pro Thr Phe
    145                150                155                160
ctg tat gcc atg cca tt 497
Leu Tyr Ala Met Pro
                165

```

```

<210> 42
<211> 165
<212> PRT
<213> Daucus carota

```

```

<400> 42
Tyr Gly Val Trp Val Asp Glu Phe Ile Asp Leu Gly Leu Glu Gly Cys
  1          5          10          15
Ile Glu His Val Trp Arg Asp Thr Ile Val Tyr Leu Asp Asp Gly Asp
    20          25          30
Pro Ile Met Ile Gly Arg Ala Tyr Gly Arg Val Ser Arg His Leu Leu
    35          40          45
His Glu Glu Leu Leu Lys Arg Cys Val Glu Ser Gly Val Ser Tyr Leu
    50          55          60
Ser Ser Lys Val Glu Lys Ile Ile Glu Ala Gly Asp Gly His Ser Leu
    65          70          75          80
Val Glu Cys Glu Asn Asn Ile Val Ile Pro Cys Arg Leu Ala Thr Val
    85          90          95
Ala Ser Gly Ala Ala Ser Gly Lys Leu Leu Gln Tyr Glu Val Gly Gly
    100          105          110
Pro Arg Val Ser Val Gln Thr Ala Tyr Gly Val Glu Val Glu Val Glu
    115          120          125
Asn Asn Pro Tyr Asp Pro Ser Leu Met Val Phe Met Asp Tyr Arg Asp
    130          135          140
Tyr Thr Lys Gln Lys Val Pro Gly Met Glu Ala Glu Tyr Pro Thr Phe
    145          150          155          160
Leu Tyr Ala Met Pro
                165

```

```

<210> 43
<211> 605
<212> DNA
<213> Daucus carota

```

```

<220>
<221> CDS
<222> (3)..(605)
<223> coding for episilon-cyclase (partial)

```

```

<400> 43
tc att ggc cgt gct tat gga aga tta gtc gcc att tgc ttc atg aag 47
Ile Gly Arg Ala Tyr Gly Arg Leu Val Ala Ile Cys Phe Met Lys
  1          5          10          15
aat tgc tta aaa ggt gtg tcg agt cag gtg ttt cgt atc tta gct caa 95
Asn Cys Leu Lys Gly Val Ser Ser Gln Val Phe Arg Ile Leu Ala Gln
    20          25          30

```



```

aag ttg aaa aga tta ttg aag ctg gag atg gcc aca gcc tgg ttg agt 143
Lys Leu Lys Arg Leu Leu Lys Leu Glu Met Ala Thr Ala Trp Leu Ser
      35              40              45
gtg aaa ata ata ttg tca ttc cat gca ggc ttg cta ctg ttg cat ctg 191
Val Lys Ile Ile Leu Ser Phe His Ala Gly Leu Leu Leu Leu His Leu
      50              55              60
gag cag ctt ctg gga aac ttt tgc agt atg ggg ttg ggg gtc cca gag 239
Glu Gln Leu Leu Gly Asn Phe Cys Ser Met Gly Leu Gly Val Pro Glu
      65              70              75
ttt ctg tcc aaa cag ctt atg gtg tgc agg ttg agg tgg aaa cca atc 287
Phe Leu Ser Lys Gln Leu Met Val Ser Arg Leu Arg Trp Lys Pro Ile
      80              85              90              95
cca tat gat ccc agt cta atg gtt ttc atg gat tac aga gat tat acc 335
Pro Tyr Asp Pro Ser Leu Met Val Phe Met Asp Tyr Arg Asp Tyr Thr
      100              105              110
aaa caa aaa gtt cca ggc atg gag gca gaa tat cca aca ttt ctt tat 383
Lys Gln Lys Val Pro Gly Met Glu Ala Glu Tyr Pro Thr Phe Leu Tyr
      115              120              125
gtg atg ccc atg tcc cca aca agg att ttc ttt gag gag aca tgt ttg 431
Val Met Pro Met Ser Pro Thr Arg Ile Phe Phe Glu Glu Thr Cys Leu
      130              135              140
gct tca aaa gat gcg atg cca ttc gat cta ctg aag aaa aaa ctc atg 479
Ala Ser Lys Asp Ala Met Pro Phe Asp Leu Leu Lys Lys Lys Leu Met
      145              150              155
tca aga tta cag acg atg gga att cga gtt gcc aag aca tat gaa gag 527
Ser Arg Leu Gln Thr Met Gly Ile Arg Val Ala Lys Thr Tyr Glu Glu
      160              165              170              175
gaa tgg tct tat ata cct gtt ggg gga tct tta cct aat act gag caa 575
Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser Leu Pro Asn Thr Glu Gln
      180              185              190
aag aat ctc gcc ttt ggt gct gcc gct aga 605
Lys Asn Leu Ala Phe Gly Ala Ala Ala Arg
      195              200

```

<210> 44
 <211> 201
 <212> PRT
 <213> Daucus carota

```

<400> 44
Ile Gly Arg Ala Tyr Gly Arg Leu Val Ala Ile Cys Phe Met Lys Asn
  1          5          10          15
Cys Leu Lys Gly Val Ser Ser Gln Val Phe Arg Ile Leu Ala Gln Lys
      20          25          30
Leu Lys Arg Leu Leu Lys Leu Glu Met Ala Thr Ala Trp Leu Ser Val
      35          40          45
Lys Ile Ile Leu Ser Phe His Ala Gly Leu Leu Leu Leu His Leu Glu
      50          55          60
Gln Leu Leu Gly Asn Phe Cys Ser Met Gly Leu Gly Val Pro Glu Phe
      65          70          75          80
Leu Ser Lys Gln Leu Met Val Ser Arg Leu Arg Trp Lys Pro Ile Pro
      85          90          95
Tyr Asp Pro Ser Leu Met Val Phe Met Asp Tyr Arg Asp Tyr Thr Lys
      100          105          110
Gln Lys Val Pro Gly Met Glu Ala Glu Tyr Pro Thr Phe Leu Tyr Val
      115          120          125
Met Pro Met Ser Pro Thr Arg Ile Phe Phe Glu Glu Thr Cys Leu Ala
      130          135          140

```

Ser Lys Asp Ala Met Pro Phe Asp Leu Leu Lys Lys Lys Leu Met Ser
 145 150 155 160
 Arg Leu Gln Thr Met Gly Ile Arg Val Ala Lys Thr Tyr Glu Glu Glu
 165 170 175
 Trp Ser Tyr Ile Pro Val Gly Gly Ser Leu Pro Asn Thr Glu Gln Lys
 180 185 190
 Asn Leu Ala Phe Gly Ala Ala Ala Arg
 195 200

<210> 45

<211> 1697

<212> DNA

<213> *Lycopersicon esculentum*

<220>

<221> CDS

<222> (6)..(1583)

<223> coding for epsilon-cyclase

<400> 45

ttgaa atg gag tgt gtt gga gtt caa aat gtt gga gca atg gca gtt tta 50
 Met Glu Cys Val Gly Val Gln Asn Val Gly Ala Met Ala Val Leu
 1 5 10 15
 acg cgt ccg aga ttg aac cgt tgg tcg gga gga gag tta tgc caa gaa 98
 Thr Arg Pro Arg Leu Asn Arg Trp Ser Gly Gly Glu Leu Cys Gln Glu
 20 25 30
 aaa agc atc ttt ttg gcg tat gag cag tat gaa agt aaa tgt aat agc 146
 Lys Ser Ile Phe Leu Ala Tyr Glu Gln Tyr Glu Ser Lys Cys Asn Ser
 35 40 45
 agt agt ggt agt gac agt tgt gta gtt gat aaa gaa gat ttt gct gat 194
 Ser Ser Gly Ser Asp Ser Cys Val Val Asp Lys Glu Asp Phe Ala Asp
 50 55 60
 gaa gaa gat tat ata aaa gcc ggt ggt tcg caa ctt gta ttt gtt caa 242
 Glu Glu Asp Tyr Ile Lys Ala Gly Gly Ser Gln Leu Val Phe Val Gln
 65 70 75
 atg cag cag aaa aaa gat atg gat cag cag tct aag ctt tct gat gag 290
 Met Gln Gln Lys Lys Asp Met Asp Gln Gln Ser Lys Leu Ser Asp Glu
 80 85 90 95
 tta cga caa ata tct gct gga caa acc gta ctg gat tta gtg gta atc 338
 Leu Arg Gln Ile Ser Ala Gly Gln Thr Val Leu Asp Leu Val Val Ile
 100 105 110
 ggc tgt ggt cct gct ggt ctt gct ctt gcc gcg gag tca gct aaa ttg 386
 Gly Cys Gly Pro Ala Gly Leu Ala Leu Ala Ala Glu Ser Ala Lys Leu
 115 120 125
 ggg ttg aac gtg ggg ctc gtt ggg cct gat ctt cct ttc aca aac aac 434
 Gly Leu Asn Val Gly Leu Val Gly Pro Asp Leu Pro Phe Thr Asn Asn
 130 135 140
 tat ggt gta tgg gag gac gag ttc aaa gat ctt ggt ctt caa gcc tgc 482
 Tyr Gly Val Trp Glu Asp Glu Phe Lys Asp Leu Gly Leu Gln Ala Cys
 145 150 155
 att gaa cat gtt tgg cgg gat acc att gta tat ctt gat gat gat gaa 530
 Ile Glu His Val Trp Arg Asp Thr Ile Val Tyr Leu Asp Asp Asp Glu
 160 165 170 175
 cct att ctt att ggc cgt gcc tat gga aga gtt agt cgc cat ttt ctg 578
 Pro Ile Leu Ile Gly Arg Ala Tyr Gly Arg Val Ser Arg His Phe Leu
 180 185 190
 cac gag gag tta ctc aaa agg tgt gtg gag gca ggt gtt ttg tat cta 626
 His Glu Glu Leu Leu Lys Arg Cys Val Glu Ala Gly Val Leu Tyr Leu

195				200				205									
aac	tcg	aaa	gtg	gat	agg	att	gtt	gag	gcc	aca	aat	ggc	cag	agt	ctt	674	
Asn	Ser	Lys	Val	Asp	Arg	Ile	Val	Glu	Ala	Thr	Asn	Gly	Gln	Ser	Leu		
210				215				220									
gta	gag	tgc	gaa	ggg	gat	gtt	gtg	att	ccc	tgc	agg	ttt	gtg	act	gtt	722	
Val	Glu	Cys	Glu	Gly	Asp	Val	Val	Ile	Pro	Cys	Arg	Phe	Val	Thr	Val		
225				230				235									
gca	tcg	ggg	gca	gcc	tcg	ggg	aaa	ttc	ttg	cag	tat	gag	ttg	gga	agt	770	
Ala	Ser	Gly	Ala	Ala	Ser	Gly	Lys	Phe	Leu	Gln	Tyr	Glu	Leu	Gly	Ser		
240				245				250				255					
cct	aga	gtt	tct	gtt	caa	aca	gct	tat	gga	gtg	gaa	gtt	gag	gtt	gat	818	
Pro	Arg	Val	Ser	Val	Gln	Thr	Ala	Tyr	Gly	Val	Glu	Val	Glu	Val	Asp		
260				265				270									
aac	aat	cca	ttt	gac	ccg	agc	ctg	atg	gtt	ttc	atg	gat	tat	aga	gat	866	
Asn	Asn	Pro	Phe	Asp	Pro	Ser	Leu	Met	Val	Phe	Met	Asp	Tyr	Arg	Asp		
275				280				285									
tat	ctc	aga	cac	gac	gct	caa	tct	tta	gaa	gct	aaa	tat	cca	aca	ttt	914	
Tyr	Leu	Arg	His	Asp	Ala	Gln	Ser	Leu	Glu	Ala	Lys	Tyr	Pro	Thr	Phe		
290				295				300									
ctt	tat	gcc	atg	ccc	atg	tct	cca	aca	cga	gtc	ttt	ttc	gag	gaa	act	962	
Leu	Tyr	Ala	Met	Pro	Met	Ser	Pro	Thr	Arg	Val	Phe	Phe	Glu	Glu	Thr		
305				310				315									
tgt	ttg	gct	tca	aaa	gat	gca	atg	cca	ttc	gat	ctg	tta	aag	aaa	aaa	1010	
Cys	Leu	Ala	Ser	Lys	Asp	Ala	Met	Pro	Phe	Asp	Leu	Leu	Lys	Lys	Lys		
320				325				330				335					
ctg	atg	cta	cga	ttg	aac	acc	ctt	ggg	gta	aga	att	aaa	gaa	att	tac	1058	
Leu	Met	Leu	Arg	Leu	Asn	Thr	Leu	Gly	Val	Arg	Ile	Lys	Glu	Ile	Tyr		
340				345				350									
gag	gag	gaa	tgg	tct	tac	ata	ccg	gtt	ggg	gga	tct	ttg	cca	aat	aca	1106	
Glu	Glu	Glu	Trp	Ser	Tyr	Ile	Pro	Val	Gly	Gly	Ser	Leu	Pro	Asn	Thr		
355				360				365									
gaa	caa	aaa	aca	ctt	gca	ttt	ggg	gct	gct	gct	agc	atg	gtt	cat	cca	1154	
Glu	Gln	Lys	Thr	Leu	Ala	Phe	Gly	Ala	Ala	Ala	Ser	Met	Val	His	Pro		
370				375				380									
gcc	aca	ggg	tat	tca	gtc	gtc	aga	tca	ctt	tct	gaa	gct	cca	aaa	tgc	1202	
Ala	Thr	Gly	Tyr	Ser	Val	Arg	Ser	Leu	Ser	Glu	Ala	Pro	Lys	Cys			
385				390				395									
gcc	tct	gta	ctt	gca	aat	ata	tta	cga	caa	cat	tat	agc	aag	aac	atg	1250	
Ala	Ser	Val	Leu	Ala	Asn	Ile	Leu	Arg	Gln	His	Tyr	Ser	Lys	Asn	Met		
400				405				410				415					
ctt	acc	agt	tca	agt	atc	ccg	agt	ata	tca	act	caa	gct	tgg	aac	act	1298	
Leu	Thr	Ser	Ser	Ser	Ile	Pro	Ser	Ile	Ser	Thr	Gln	Ala	Trp	Asn	Thr		
420				425				430									
ctt	tgg	cca	caa	gaa	cga	aaa	cga	caa	aga	tcg	ttt	ttc	cta	ttt	gga	1346	
Leu	Trp	Pro	Gln	Glu	Arg	Lys	Arg	Gln	Arg	Ser	Phe	Phe	Leu	Phe	Gly		
435				440				445									
ctg	gct	ctg	ata	ttg	cag	ctg	gat	att	gag	ggg	ata	agg	tca	ttt	ttc	1394	
Leu	Ala	Leu	Ile	Leu	Gln	Leu	Asp	Ile	Glu	Gly	Ile	Arg	Ser	Phe	Phe		
450				455				460									
cgc	gca	ttc	ttc	cgt	gtg	cca	aaa	tgg	atg	tgg	cag	gga	ttt	ctt	ggg	1442	
Arg	Ala	Phe	Phe	Arg	Val	Pro	Lys	Trp	Met	Trp	Gln	Gly	Phe	Leu	Gly		
465				470				475									
tca	agt	ctt	tct	tca	gca	gac	ctc	atg	tta	ttt	gcc	ttc	tac	atg	ttt	1490	
Ser	Ser	Leu	Ser	Ser	Ala	Asp	Leu	Met	Leu	Phe	Ala	Phe	Tyr	Met	Phe		
480				485				490				495					
att	att	gca	cca	aat	gac	atg	aga	aaa	ggc	ttg	atc	aga	cat	ctt	tta	1538	
Ile	Ile	Ala	Pro	Asn	Asp	Met	Arg	Lys	Gly	Leu	Ile	Arg	His	Leu	Leu		
500				505				510									
tct	gat	cct	act	ggg	gca	aca	ttg	ata	aga	act	tat	ctt	aca	ttt		1583	
Ser	Asp	Pro	Thr	Gly	Ala	Thr	Leu	Ile	Arg	Thr	Tyr	Leu	Thr	Phe			

515 520 525
 tagagtaaac tcctcctaca ataattgttg aatcagagggc ctcattactt cagattcata 1643
 acagaaatcg cgggtctctcg aggcatttgta tataacattt tcactagctt aata 1697

<210> 46
 <211> 526
 <212> PRT
 <213> *Lycopersicon esculentum*

<400> 46
 Met Glu Cys Val Gly Val Gln Asn Val Gly Ala Met Ala Val Leu Thr
 1 5 10 15
 Arg Pro Arg Leu Asn Arg Trp Ser Gly Gly Glu Leu Cys Gln Glu Lys
 20 25 30
 Ser Ile Phe Leu Ala Tyr Glu Gln Tyr Glu Ser Lys Cys Asn Ser Ser
 35 40 45
 Ser Gly Ser Asp Ser Cys Val Val Asp Lys Glu Asp Phe Ala Asp Glu
 50 55 60
 Glu Asp Tyr Ile Lys Ala Gly Gly Ser Gln Leu Val Phe Val Gln Met
 65 70 75 80
 Gln Gln Lys Lys Asp Met Asp Gln Gln Ser Lys Leu Ser Asp Glu Leu
 85 90 95
 Arg Gln Ile Ser Ala Gly Gln Thr Val Leu Asp Leu Val Val Ile Gly
 100 105 110
 Cys Gly Pro Ala Gly Leu Ala Leu Ala Ala Glu Ser Ala Lys Leu Gly
 115 120 125
 Leu Asn Val Gly Leu Val Gly Pro Asp Leu Pro Phe Thr Asn Asn Tyr
 130 135 140
 Gly Val Trp Glu Asp Glu Phe Lys Asp Leu Gly Leu Gln Ala Cys Ile
 145 150 155 160
 Glu His Val Trp Arg Asp Thr Ile Val Tyr Leu Asp Asp Asp Glu Pro
 165 170 175
 Ile Leu Ile Gly Arg Ala Tyr Gly Arg Val Ser Arg His Phe Leu His
 180 185 190
 Glu Glu Leu Leu Lys Arg Cys Val Glu Ala Gly Val Leu Tyr Leu Asn
 195 200 205
 Ser Lys Val Asp Arg Ile Val Glu Ala Thr Asn Gly Gln Ser Leu Val
 210 215 220
 Glu Cys Glu Gly Asp Val Val Ile Pro Cys Arg Phe Val Thr Val Ala
 225 230 235 240
 Ser Gly Ala Ala Ser Gly Lys Phe Leu Gln Tyr Glu Leu Gly Ser Pro
 245 250 255
 Arg Val Ser Val Gln Thr Ala Tyr Gly Val Glu Val Glu Val Asp Asn
 260 265 270
 Asn Pro Phe Asp Pro Ser Leu Met Val Phe Met Asp Tyr Arg Asp Tyr
 275 280 285
 Leu Arg His Asp Ala Gln Ser Leu Glu Ala Lys Tyr Pro Thr Phe Leu
 290 295 300
 Tyr Ala Met Pro Met Ser Pro Thr Arg Val Phe Phe Glu Glu Thr Cys
 305 310 315 320
 Leu Ala Ser Lys Asp Ala Met Pro Phe Asp Leu Leu Lys Lys Lys Leu
 325 330 335
 Met Leu Arg Leu Asn Thr Leu Gly Val Arg Ile Lys Glu Ile Tyr Glu
 340 345 350
 Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser Leu Pro Asn Thr Glu
 355 360 365
 Gln Lys Thr Leu Ala Phe Gly Ala Ala Ala Ser Met Val His Pro Ala
 370 375 380

```

Thr Gly Tyr Ser Val Val Arg Ser Leu Ser Glu Ala Pro Lys Cys Ala
385                      390                      395                      400
Ser Val Leu Ala Asn Ile Leu Arg Gln His Tyr Ser Lys Asn Met Leu
                      405                      410                      415
Thr Ser Ser Ser Ile Pro Ser Ile Ser Thr Gln Ala Trp Asn Thr Leu
                      420                      425                      430
Trp Pro Gln Glu Arg Lys Arg Gln Arg Ser Phe Phe Leu Phe Gly Leu
                      435                      440                      445
Ala Leu Ile Leu Gln Leu Asp Ile Glu Gly Ile Arg Ser Phe Phe Arg
                      450                      455                      460
Ala Phe Phe Arg Val Pro Lys Trp Met Trp Gln Gly Phe Leu Gly Ser
465                      470                      475                      480
Ser Leu Ser Ser Ala Asp Leu Met Leu Phe Ala Phe Tyr Met Phe Ile
                      485                      490                      495
Ile Ala Pro Asn Asp Met Arg Lys Gly Leu Ile Arg His Leu Leu Ser
                      500                      505                      510
Asp Pro Thr Gly Ala Thr Leu Ile Arg Thr Tyr Leu Thr Phe
                      515                      520                      525

```

```

<210> 47
<211> 510
<212> DNA
<213> Tagetes erecta

<220>
<221> misc_feature
<222> (1)..(510)
<223> coding for epsilon-cyclase specific probe

```

```

<400> 47
ggcacgaggc aaagcaaagg ttgtttgttg ttgttggtga gagacactcc aatccaaaca 60
gatacaaggc gtgactggat atttctctct cgttcctaac aacagcaacg aagaagaaaa 120
agaatcatta ctaacaatca atgagtatga gagctggaca catgacggca acaatggcgg 180
cttttacatg ccctagggtt atgactagca tcagatacac gaagcaaatt aagtgcaacg 240
ctgctaaaag ccagctagtc gttaaacaag agattgagga ggaagaagat tatgtgaaag 300
cgggtggatc ggagctgctt tttgttcaaa tgcaacagaa taagtccatg gatgcacagt 360
ctagcctatc ccaaaagctc ccaaggggtac caataggagg aggaggagac agtaactgta 420
tactggattt gggttgtaatt gggttggtgc ctgctggcct tgctcttgct ggagaatcag 480
ccaagctagg cttgaatgtc gcacttatcg                               510

```

```

<210> 48
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
        oligonucleotide primer

```

```

<400> 48
ggcacgaggc aaagcaaagg

```

20

```

<210> 49
<211> 21
<212> DNA

```

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
oligonucleotide primer

<400> 49

cgataagtgc gacattcaag c

21

<210> 50

<211> 734

<212> DNA

<213> Tagetes erecta

<220>

<221> misc_feature

<222> (1)..(734)

<223> fragment of epsilon cyclase gene obtain by iPCR
comprising part of promoter region

<400> 50

```
ctaacaatca atgagtagag agctggacac atgacggcaa caatggcggc ttttacaatgc 60
cctaggttta tgactagcat cagatacacg aagcaaatta agtgcaacgc tgctaaaagc 120
cagctagtcg ttaaacaaga gattgaggag gaagaagatt atgtgaaagc cgggtggatcg 180
gagctgcttt ttgttcaa atgcaacagaat aagtccatgg atgcacagtc tagcctatcc 240
caaaagggtca ctccagactt aattgcttat aaataaataa atatgttttt taggaataat 300
gatattttaga tagattagct atcacctgtg ctgtgggtgtg cagctcccaa ggggtcttacc 360
gatagtaaaa tcgttagtta tgattaatac ttggggagggtg ggggattata ggctttgttg 420
tgagaatggt gagaaagagg tttgacaaat cgggtgtttga atgagggttaa atggagttaa 480
attaaaataa agagaagaga aagattaaga ggggtgatggg gatattaaag acggscaata 540
tagtgatgcc acgtagaaaa aggtaagtga aaacatacaa cgtggcttta aaagatggct 600
tggctgctaa tcaactcaac tcaactcata tcctatccat tcaaattcaa ttcaattcta 660
ttgaatgcaa agcaaagcaa aggttggttg ttgttggttg tgagagacac tccaatccaa 720
acagatacaa ggcg
```

734

<210> 51

<211> 280

<212> DNA

<213> Tagetes erecta

<220>

<221> misc_feature

<222> (1)..(280)

<223> fragment of epsilon cyclase gene obtain by
TAIL-PCR comprising part of promoter region

<400> 51

```
gtcgagtatg gagttcaatt aaaataaaga gaagaraaag attaagaggg tgatggggat 60
attaaagacg gccaatrtag tgatgccacg taagaaaaag gtaagtgaac acatacaacg 120
tggctttaaa agatgggcttg gctgctaate aactcaactc aactcatatc ctatccattc 180
aaattcaatt caattctatt gaatgcaaag caaagcaaag caaagggttg ttgttggttg 240
tgttgagaga cactccaatc caaacagata caaggcgtga
```

280

<210> 52

<211> 23
 <212> DNA
 <213> Artificial sequence

<220>

<223> Description of the artificial sequence:
 oligonucleotide primer

<400> 52
 cgccttgat ctgtttggat tgg

23

<210> 53
 <211> 24
 <212> DNA
 <213> Artificial sequence

<220>

<223> Description of the artificial sequence:
 oligonucleotide primer

<400> 53
 ctaacaatca atgagtatga gagc

24

<210> 54
 <211> 26
 <212> DNA
 <213> Artificial sequence

<220>

<223> Description of the artificial sequence:
 oligonucleotide primer

<400> 54
 agagcaaggc cagcaggacc acaacc

26

<210> 55
 <211> 26
 <212> DNA
 <213> Artificial sequence

<220>

<223> Description of the artificial sequence:
 oligonucleotide primer

<400> 55
 ccttgaggagc ttttgggata ggctag

26

<210> 56
 <211> 26
 <212> DNA
 <213> Artificial sequence

<220>

<223> Description of the artificial sequence:
oligonucleotide primer

<400> 56

tcacgccttg tatctgtttg gattgg

26

<210> 57

<211> 15

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
oligonucleotide primer

<400> 57

gtcgagtatg gagtt

15

<210> 58

<211> 734

<212> DNA

<213> Tagetes erecta

<220>

<221> misc_feature

<222> (1)..(734)

<223> coding for epsilon-cyclase genomic iPCR-fragment

<400> 58

```
ctaacaatca atgagtagag agctggacac atgacggcaa caatggcggc ttttacatgc 60
cctaggttta tgactagcat cagatacacg aagcaaatta agtgcaacgc tgctaaaagc 120
cagctagtcg ttaaacaaga gattgaggag gaagaagatt atgtgaaagc cgggtggatcg 180
gagctgcttt ttgttcaa atgcaacagaat aagtccatgg atgcacagtc tagcctatcc 240
caaaagggtca ctccagactt aattgcttat aaataaataa atatgttttt taggaataat 300
gatattttaga tagattagct atcacctgtg ctgtgggtgtg cagctcccaa ggggtcttacc 360
gatagtaaaa tcgttagtta tgattaatac ttgggagggtg ggggattata ggctttgttg 420
tgagaatgtt gagaaagagg ttgacaaat cgggtgtttga atgagggttaa atggagttaa 480
attaaaataa agagaagaga aagattaaga ggggtgatggg gatattaaag acggscaata 540
tagtgatgcc acgtagaaaa aggtaagtga aaacatacaa cgtggcttta aaagatggct 600
tggctgctaa tcaactcaac tcaactcata tcctatccat tcaaattcaa ttcaattcta 660
ttgaatgcaa agcaaagcaa aggttggttg ttgttggtgt tgagagacac tccaatccaa 720
acagatacaa ggcg
```

734

<210> 59

<211> 25

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
oligonucleotide primer

<400> 59
ctcgagagta aaatcgttag ttatg 25

<210> 60
<211> 29
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
oligonucleotide primer

<400> 60
ccatggccat tgattgtag taatgattc 29

<210> 61
<211> 29
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
oligonucleotide primer

<400> 61
ccatggtaat ttgcttcgtg tatctgatg 29

<210> 62
<211> 26
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
oligonucleotide primer

<400> 62
ccatggcgct agcagcgaca gtaatg 26

<210> 63
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
oligonucleotide primer

<400> 63
gatatccggt gtgagggaac tag 23

<210> 64
 <211> 22
 <212> DNA
 <213> Artificial sequence

<220>

<223> Description of the artificial sequence:
 oligonucleotide primer

<400> 64
 gcaagctcga cagctacaaa cc

22

<210> 65
 <211> 24
 <212> DNA
 <213> Artificial sequence

<220>

<223> Description of the artificial sequence:
 oligonucleotide primer

<400> 65
 gaagcatgca gctagcagcg acag

24

<210> 66
 <211> 1795
 <212> DNA
 <213> Artificial sequence

<220>

<223> Description of the artificial sequence: coding for
 ketolase - 35S terminator construct

<400> 66
 ccatggcgct agcagcgaca gtaatgttgg agcagcttac cggaagcgct gaggcactca 60
 aggagaagga gaaggaggtt gcaggcagct ctgacgtgtt gcgtacatgg gcgacccagt 120
 actcgcttcc gtcagaggag tcagacgcgg ccgcccggg actgaagaat gcctacaagc 180
 caccaccttc cgacacaaaag ggcatacaca tggcgctagc tgtcatcggc tcctgggccc 240
 cagtgttccct ccacgccatt tttcaaatca agcttccgac ctcttggac cagctgcact 300
 ggctgcccgt gtcagatgcc acagctcagc tggttagcgg cagcagcagc ctgctgcaca 360
 tcgtcgtagt attctttgtc ctggagttcc tgtacacagg cttttttatc accacgcatg 420
 atgctatgca tggcaccatc gccatgagaa acaggcagct taatgacttc ttgggcagag 480
 tatgcatctc cttgtacgcc tggtttgatt acaacatgct gcaccgcaag cattggggagc 540
 accacaacca cactggcgag gtgggcaagg accctgactt ccacagggga aaccctggca 600
 ttgtgccctg gtttgccagc ttcatgtcca gctacatgtc gatgtggcag tttgcgcgcc 660
 tcgcatgggtg gacgggtggtc atgcagctgc tgggtgcgcc aatggcgaa ctgctgggtgt 720
 tcatggcggc cgcgcccatc ctgtccgcct tccgcttgtt ctactttggc acgtacatgc 780
 cccacaagcc tgagcctggc gccgcgtcag gctcttcacc agccgtcatg aactgggtgga 840
 agtcgcgcac tagccaggcg tccgacctgg gacctttct gacctgctac cacttcgacc 900
 tgcactggga gcaccaccgc tggccctttg ccccttggtg ggagctgccc aactgccgcc 960
 gcctgtctgg ccgaggtctg gttcctgcct agctggacac actgcagtgg gccctgctgc 1020
 cagctgggca tgccctgcagg tcgacggatc ccgggaatt cggtacgctg aaatcaccag 1080
 tctctctcta caaatctatc tctctctatt ttctccataa ataatgtgtg agtagtttcc 1140
 cgataagggga aattaggggt cttatagggg ttgcgtcatg tgttgagcat ataagaaacc 1200
 cttagtatgt atttgtattt gtaaaatact tctatcaata aaattttctaa ttcctaaaac 1260

```

caaaatccag tactaaaatc cagatctcct aaagtcccta tagatctttg tcgtgaatat 1320
aaaccagaca cgagacgact aaacctggag ccagagcgcc gttcgaagct agaagtaccg 1380
cttaggcagg aggcggttag ggaaaagatg ctaaggcagg gttggttacg ttgactcccc 1440
cgtaggtttg gtttaaatat gatgaagtgg acggaaggaa ggaggaagac aaggaaggat 1500
aaggttgcag gccctgtgca aggtagaag atggaaattt gatagaggta cgctactata 1560
cttatactat acgctaaggg aatgcttgta ttataaccct ataccacctt ataaccctt 1620
atcaatttaa gaaataatcc gcataagccc ccgcttaaaa attggtatca gagccatgaa 1680
taggtctatg accaaaactc aagaggataa aacctcacca aaatacgaaa gagttcttaa 1740
ctctaaagat aaaagatctt tcaagatcaa aactagttcc ctcacaccgg atatac 1795

```

```

<210> 67
<211> 28
<212> DNA
<213> Artificial sequence

```

```

<220>
<223> Description of the artificial sequence:
        oligonucleotide primer

```

```

<400> 67
gagctcactc actgatttcc attgcttg                                     28

```

```

<210> 68
<211> 37
<212> DNA
<213> Artificial sequence

```

```

<220>
<223> Description of the artificial sequence:
        oligonucleotide primer

```

```

<400> 68
cgccgttaag tcgatgtccg ttgatttaaa cagtgtc                                     37

```

```

<210> 69
<211> 34
<212> DNA
<213> Artificial sequence

```

```

<220>
<223> Description of the artificial sequence:
        oligonucleotide primer

```

```

<400> 69
atcaacggac atcgacttaa cggcgtttgt aaac                                     34

```

```

<210> 70
<211> 25
<212> DNA
<213> Artificial sequence

```

```

<220>
<223> Description of the artificial sequence:
        oligonucleotide primer

```

<400> 70
 taagcttttt gttgaagaga tttgg 25

<210> 71
 <211> 28
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:
 oligonucleotide primer

<400> 71
 gtcgactacg taagtttctg cttctacc 28

<210> 72
 <211> 26
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:
 oligonucleotide primer

<400> 72
 ggatccggtg atacctgcac atcaac 26

<210> 73
 <211> 28
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:
 oligonucleotide primer

<400> 73
 aagcttaccg atagtaaaat cgtagtt 28

<210> 74
 <211> 31
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:
 oligonucleotide primer

<400> 74
 ctcgagctta ccgatagtaa aatcgtagt t 31

<210> 75
 <211> 28
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:
 oligonucleotide primer

<400> 75
 gtcgacaaca acaacaaaca acctttgc 28

<210> 76
 <211> 28
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:
 oligonucleotide primer

<400> 76
 ggatccaaca acaacaaaca acctttgc 28

<210> 77
 <211> 777
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> promoter
 <222> (1)..(777)
 <223> modified version of the AP3 promoter

<400> 77
 gagctcactc actgatttcc attgcttgaa aattgatgat gaactaagat caatccatgt 60
 tagtttcaaa acaacagtaa ctgtggccaa cttagttttg aaacaacact aactgggtcga 120
 agcaaaaaga aaaaagagtt tcatcatata tctgatttga tggactgttt ggagtttagga 180
 ccaaacatta tctacaaaca aagacttttc tcctaacttg tgattccttc ttaaacccta 240
 ggggtaatat tctattttcc aaggatcttt agttaaaggc aaatccggga aattattgta 300
 atcatttggg gaaacatata aaagatttga gttagatgga agtgacgatt aatccaaaca 360
 tatatatctc tttcttctta tttcccaaat taacagacaa aagtagaata ttggctttta 420
 acaccaatat aaaaacttgc ttcacaccta aacacttttg tttactttag ggtaagtgc 480
 aaaagccaac caaatccacc tgcactgatt tgacgtttac aaacgccgtt aagtcgatgt 540
 ccgttgattt aaacagtgtc ttgtaattaa aaaaatcagt ttacataaat ggaaaattta 600
 tcacttagtt ttcatcaact tctgaactta cttttcatgg attaggcaat actttccatt 660
 tttagtaact caagtggacc ctttacttct tcaactccat ctctctcttt ctatttcact 720
 tctttcttct cattatatct cttgtcctct ccaccaaata tcttcaacaa aaagctt 777

<210> 78
 <211> 212
 <212> DNA
 <213> Solanum tuberosum

<220>
 <221> intron
 <222> (1)..(212)
 <223> PIV2 intron of ST-LS1 gene

<400> 78
 gtcgactacg taagtttctg cttctacctt tgatatatat ataataatta tcattaatta 60
 gtagtaatat aatatttcaa atattttttt caaaataaaa gaatgtagta tatagcaatt 120
 gcttttctgt agtttataag tgtgtatatt ttaatttata acttttctaa tatatgacca 180
 aaatttggtg atgtgcagg atcaccggat cc 212

<210> 79
 <211> 358
 <212> DNA
 <213> *Tagetes erecta*

<220>
 <221> misc_feature
 <222> (1)..(358)
 <223> coding for sense-strand of epsilon cyclase
 promoter directed dsRNA

<400> 79
 aagcttaccg atagtaaaat cgtaggttat gattaatact tgggaggtgg gggattatag 60
 gctttgttgt gagaatgttg agaaagaggt ttgacaaatc ggtgtttgaa tgaggttaaa 120
 tggagtttaa ttaaaataaa gagaagagaa agattaagag ggtgatgggg atattaaaga 180
 cggccaatat agtgatgcca cgtagaaaaa ggtaagtga aacatacaac gtggctttta 240
 aagatggctt ggctgcta atcaactcaact caactcatat cctatccatt caaattcaat 300
 tcaattctat tgaatgcaaa gcaaagcaaa gcaaaggttg tttgttggtg ttgtcgac 358

<210> 80
 <211> 361
 <212> DNA
 <213> *Tagetes erecta*

<220>
 <221> misc_feature
 <222> (1)..(361)
 <223> coding for antisense-strand of epsilon cyclase
 promoter directed dsRNA

<400> 80
 ctcgagctta ccgatagtaa aatcgtagt tatgattaat acttgggagg tgggggatta 60
 taggctttgt tgtgagaatg ttgagaaaga ggtttgacaa atcgggtgtt gaatgaggtt 120
 aaatggagtt taattaaaaa aaagagaaga gaaagattaa gagggatgat gggatattaa 180
 agacggccaa tatagtgatg ccacgtagaa aaaggtaagt gaaaacatac aacgtggctt 240
 taaaagatgg cttggctgct aatcaactca actcaactca tctctatcc attcaaattc 300
 aattcaattc tattgaatgc aaagcaaagc aaagcaaagg ttgtttgttg ttgttgatc 360
 c 361

<210> 81
 <211> 1537
 <212> DNA
 <213> *Cucumis sativus*

<220>
 <221> promoter
 <222> (1)..(1537)
 <223> promoter of chromoplast-specific
 carotenoid-associated protein (CHRC)

<400> 81
 gagctctaca aattaggggtt actttatttca ttttcatcca ttctctttat tgttaaattt 60
 tgtacattta ttcaataata ttatatgttt attacaaatt ctactttct tattcatacc 120
 tattcactca agcctttacc atcttccttt tctatttcaa tactatttct acttcatttt 180
 tcacgttttt aacatctttc tttatttctt gtccacttcg tttagggatg cctaagtgtc 240
 caaatttcat ctctcgtagt aacacaaaac caatgtaatg ctacttctct ctacattttt 300
 aatacaata aagtgaaca aaatatctat aaataaaca atatatatat tttgttagac 360
 gctgtctcaa cccatcaatt aaaaaatttt gttatatttc tactttacct actaaatttg 420
 tttctcatat ttacctttta acccccacaa aaaaaaatta taaaaaagaa agaaaaaagc 480
 taaaccctat ttaaatagct aactataaga tcttaaaatt atctctcatca gtgtatagtt 540
 taattgggta ttaacttata acattatata tctatgacat atactctctc ctagtattt 600
 ctacattttt ttaacttaag aaaatagtca taacatagtc taaaattcaa acatccacat 660
 gctctaattt gattaacaaa aagttagaaa tatttattta aataaaaaag actaataaat 720
 atataaaatg aatgttcata cgcagaccca tttagagatg agtatgcttt cacatgctga 780
 gattattttc aaaactaagg ttgtagcaat attaaatcaa taaaattatt ataaataaca 840
 aaattaacct gctcgtgttt gctgtatatg ggaggctaca aaataaatta aactaaagat 900
 gattatgttt tagacatttt ttctatctgt attagtttat acatattaat tcaggagctg 960
 cacaacccaa ttctattttc gttccttggt ggctgggttt ctcaacagg tcaatagtca 1020
 atattaggtt ttattggact tttaatagta tcaaacaaat ctatgtgtga acttaaaaat 1080
 tgtattaaat atttagggta acctgttgcc gtttttagaa taatgtttct tcttaataca 1140
 cgaaagcgta ttgtgtattc attcatttgg cgctcacat gcttcggttg gctcgtttta 1200
 gtctctgctt tctttgtata ttgtactccc cctcttctta tgccacgtgt tctgagctta 1260
 acaagccacg ttgctgtcca ttgccaaaca agtcatttta acttcacaag gtccgatttg 1320
 acctcaaaa caacgacaag tttccgaaca gtcgcgaaga tcaagggtat aatcgtcttt 1380
 ttgaattcta tttctcttta tttaatagtc cctctcgtgt gatagttttt aaaagatttt 1440
 taaaacgtag ctgctgttta agtaaatccc agtccttcag tttgtgcttt tgtgtgtttt 1500
 gtttctctga tttacggaat ttggaaataa taagctt 1537

<210> 82
 <211> 22
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:
 oligonucleotide primer

<400> 82
 gagctctaca aattaggggtt ac

22

<210> 83
 <211> 23
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:
 oligonucleotide primer

<400> 83 +
aagcttatta ttccaaatt ccg